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CDS	source	FEATURES	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX281582	100001
/organism="Homo saplens" /db_xref="taxon:9606" 20. 1489 /note="unnamed protein product" /codon_start=1	11647	Arexis Ab (Sb) Location/Oualifiers	Patent: WO 0177305-A 5 18-OCT-2001;	Variants of the human amp-activated protein kinase gamma 3 subunit	Andersson, L., Luthman, H. and Marklund, S.	1 (sites)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.	•	AX281582.1 GI:16608833	AX281582	0 1.	AX281582 1647 bp DNA linear PAT 02-NOV-2001		

BASE COUNT ORIGIN Query Match 100.0%; Best Local Similarity 100.0%; Matches 1647; Conservative (346 /protein_id="Cad10589.1"
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AJ249977.1 GI:6688200 AMP-activated protein

kinase;

AMPK

gamma

gene;

gamma

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subunit.

Homo sapiens numan.

RESULT : HSA249977 LOCUS DEFINITION

Homo gapiens mRNA for AMP-activated (AMPK gamma 3 gene).

mRNA protein

kinase

gamma

PRI 07-APR-2000 gamma 3 subunit

REFERENCE AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2290)
Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D.

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Direct Submission
Direct Submission
Submitted (12-OCT-1999) Carling D., Cellular Stress
Clinical Sciences Centre, Hammersmith Hospital, DuCa
London, W12 ONN, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Characterization of AMP-activated protein isoforms and their role in AMP binding blochem. J. 346 Pt 3, 659-669 (2000)
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395 gcaggctccagcacagatgatgtggagctggccacggagttcccagccacagaggcctgg 454
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2115)

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20. 1489

/note="unnamed protein product" /codon_start=1

Location/Qualifiers
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Andersson, L., Luthman, H. and Marklund, S. Variants of the human amp-activated protein kinase gamma 3 subunit Patent: wo 0177305-A 5 18-OCT-2001;

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GSLLPRPSFLYRTIGDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNEGGQV

VGLYSRFDVIHLAAQOTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIARE

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REFERENCE AUTHORS

Homo sapiens
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Mammalia; Eutheria; P
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Cheung, P.C., Salt, I.P

Chordata; Primates;

Craniata; Vertebrata; Catarrhini; Hominidae;

Euteleostomi;

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AJ249977.1 GI:6688200 AMP-activated protein human.

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AMPK

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gene;

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RESULT 2 HSA249977 LOCUS

DEFINITION

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Direct Submission
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Clinical Sciences Centre
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LVANGVBAAPLWDSKKQSFVGMLTTTDFTLVLHRYYRSPLVQITVEIEOHKIETWREIY
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Rogel-Gaillard,C., Iannuccelli,N.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
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Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
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A mutation in PRKAG3 associated with excess glycogen
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Patent: WO 0120003-A 31 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
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Sus scrofa
Eukaryota;
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Sequence
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy Chardon,P.
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/db_xref="taxon:9823"
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel Gaillard,C., Paul,S., Gellin,J., Lundstrom,K.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Constitution
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                           Submitted (10-DEC-1999) Dept Animal Breeding University of Agricultural Sciences, BMC box
                                                                                                                                                                                                                                                                             skeletal muscle
Science 288 (54)
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Sus scrofa
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   Variants of the gamma chain of ampk, dna sequences en same, and uses thereof patent: WO 012003-A 27 22-MAR-2001; INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) Andersson, Leif (SE); Looft, Christian (DE); Kalm, Location/Qualifiers
                                                 1 (bases 1 to 1873)
Andersson,L., Looft,C., Kalm,B., M.
Rogel-Galillard,C., Iannuccelli,N.,
Chardon,P.
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Eutheria; Cetartiodactyla; Suina; Suidae;
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        Andersson, L., Looft, C., Kalm, E., M. Rogel-Gaillard, C., Iannuccelli, N., Chardon, P.
Variants of the gamma chain of ampl
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Eutheria; Cetartiodactyla; Suina; Suidae;
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Andersson, Leif (SE); Looft, Christian (DE); Kalm,
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                      AMP-activated protein kinase;
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
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Characterization of AMP-activated protein kinase subunits. Assembly of the heterotrimeric complex J. Biol. Chem. 271 (17), 10282-10290 (1996)
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U42413.1
                                                                                                                                                                                                                                                                                                Witters,L.A.

Direct Submission

Direct Submission

Submitted (07-DEC-1995) Lee A. Witters, Medicine/Biochemistry,

Dartmouth Medical School, N. College St., Hanover, NH 03755-38
                                                                                                                                                                                                                                                                                                                                                                                                                         Gao,G., Fernandez,C.S., Stapleton,D., Auster,A.S., Dyck,J.R., Kemp,B.E. and Witters,L.A.
Non-catalytic beta- and gamma-subunit isoforms of 1
5'-AMP-activated protein kinase
J., Biol. Chem. 271 (15), 8675-8681 (1996)
                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 155)
Gao, G., Widmer, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/protein_id="AAC52580.1"
/db_xref="GI:133580"
/db_xref="GI:133580"
/tras1ation="SapapenehSqetpesnssvyttemkshrcydliptsskivyfd
TSLQVKKAFFALVTNGVRAAPLWDSKKOSFVGWLTITDFINILHRYYKSALVQIYELE
EHKIETWREVYLQDSFKPLVCISPNASLFDAVGSLIRNKIHRLPVIDPESGNTLYILT
HKRILKETKLETTEFFRFEFMSKSLEELQIGTYANIAWYRTTTDYVALGIFVOHRVS
ALPVVDEKGRVVDIYSKEDVINLAAEKTYNNLDVSVTKALQHSSHYFEGVLKCYLHET
LEAIINRLVEAEVHRLVVVDEHDVVKGIVSLSDILQALVLTGGEKKP"
                                                                                                                                                                                                 /organism="Rattus norvegicus"
/db_xref="taxon:10116"
<1. 972
                                                                                                                                                 subunit"
                                                                                                                                                              /codon_start=1
/product="5'-AMP-activated
                                                                                                                                                                                                                                                                    Location/Qualifiers
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gamma-1 subunit
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Murinae;
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            ttgggcgtggtctccctctccgacatccttcaggcactggtgctca 1457
                                                        gacaggattgctcggggagcaggtacacaggctggtgctagtggacgagacccagcatctc
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                                            AATAGACTGGTGGAAGCAGAGGTTCACCGTCTGGTGGTGGTGGATGAACATGACGTGGTC
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Louis

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REFERENCE
AUTHORS
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Sequence 2 from Patent W00177305.
AX281579
AX281579.1 GI:16608830
       The sequence of Homo sapiens clone 
Unpublished
                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 196554)
                                                                                                                       AC073128 196554 bp DNA 1
Homo sapiens chromosome 2 clone RP11-64705,
17 unordered pieces.
AC073128
AC073128.3 G1:13027579
AC073128.3 G1:13027579
                                     Waterston, R.H.
                                                                                             Homo sapiens
                                                                                                             human.
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Mammalia; Eutheria; Primates;
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/db_xref="taxon:9606"
306 c 286 g 16
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99.3%;
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Pred. No. 1.3e-82;
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Catarrhini;
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DRAFT SEQUENCE,
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TITLE
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                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; 98%
Sequencing vector: plasmid; 0%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 98% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 197795 bases at least Q40
Consensus quality: 190513 bases at least Q30
Consensus quality: 192099 bases at least Q20
Insert size: 200000; agarose-fp
Insert size: 194954; sum-of-contigs
Quality coverage: 5.58 in Q20 bases; sum-of-contigs
Quality coverage: 5.57 in Q20 bases; sum-of-contigs
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Submitted (08-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Feb 21, 2001 this sequence version replaced 91:8469048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 196554) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: H_NH0647005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Washington University Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                        28888
35256
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3601
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5104
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                          Location/Qualifiers
                                                                                                             28997: gap of unknown length
35255: contig of 6268 bp in le
35355 gap of unknown length
44642: contig of 9287 bp in le
44742: gap of unknown length
58275: contig of 13533 bp in l
58375: gap of unknown length
73816: contig of 15441 bp in l
73916: gap of unknown length
73916: contig of 1844 bp in l
73916: contig of 1844 bp in l
73916: contig of 1804 bp in l
73916: gap of unknown length
131337: gap of unknown length
113337: gap of unknown length
                             .196554
                                                     130425: gap of unknown length
149287: contig of 18862 bp in
149387: gap of unknown length
196554: contig of 47167 bp in
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28887
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1257: gap of unknown
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                                                                   gcctgccctgtgcctgtccccgcaggccccatttcccaagctgggctgggatgacgaact 546
                                                                                                                    CACCGAGTTCCCAGCCACAGAGGCCTGGGGAGTGTGAGCTAGAAGGCCTGCTGGAAGAGAG
                                                                                                                               cacggagttcccagccacagaggcctgggagtgtgagctagaaggcctgctggaagagag
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catggcaactagctccaagctagtcatcttcgacaccatgctggagatcaag
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/note-"assembly_name:Contig18"
3701. .5103
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113438. .130325
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8625. .11856
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1258. .
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46993 c Amon
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130426_ .149287
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Pred. No. 7.8e-83;
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Matches 581; Conservative
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                                                                                                                                                                                                                                                      tagtcatcttcgacaccatgctggagatcaagaaggccttctttgctctggtggccaacg
                                                                                                                                                                                          gtgtgcgggcagcccctctatgggacagcaagaagcagagctttgtgggggatgctgacca 746
                    agattgaacaacataagattgagacctggagggagatctacctgcaaggctgcttcaagc
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                                                                                                                                                                    GTGTTCGTGCCGCCCCTTTGTGGGACAGTAAGAAGCAGTGTTTTGTGGGCATGCTGACCA
                                                                                                                                                                                                                                                                                                                                          TGTATACTTCCTTCATGAAGTCTCATCGCTGCTATGACCTAATTCCCCACAAGTTCCAAGT 181
AACTCGAGGAGCACAAGATAGAGACGTGGAGAGGTGTACCTGCAGGACTCCTTTAAGC
                                                                                      TCACCGACTTCATCAACATTTTGCACCGATACTATAAGTCAGCCCTGGTGCAGATTTACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-DEC-1997) AG.Engel, Goettingen 37073, Germany
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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a 414 c 416 g 400 t 10 others
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43. .1035
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BC015283
BC015283.1 GI
                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site: http://www.shgc.stanford.edu
                                                                                                                                                                                  Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 3132)
                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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(Dickson, Mark) mcdepaxil.stanford.edu
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                              tcctctaccgcactatccaagatttgggcatcggcacattccgagacttggctgtggtgc 1106
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Series: IRAK Plate: 25 Row: i Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein.
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MPLLDGDVENSEKHSSRKVDSPFSSGSPSRGLFSRGPQPFPSSPVSAPVRFKTSPGSP
KTVFPFSVQESPFNSRHSSRKVDSYPFSSGSPSRGLFSRGPQPFSSSPVSAPVRFKTSPGSP
KTVFPFSVQESPFNSPFRMSFSGIFRSSSKESSPNSNPSTSPGGIRFFSRSKTSSVS
SSPSTPTQVTKQHFPLLSYKQEPERPSSRIYASSSPDTTGQRRCLAFQSPARPPLAS
SSPSTPTQTTLQVKKAFFALVANCVEAAPLÆSEKOSFVGMTTTDFINILHRYYKSPMVQ
LYFDTTLQVKKAFFALVANCVEAAPLÆSKKOSFVGMTTTDFINILHRYYKSPMVQ
IYFLEEHKIETTWRELVLQETFKRUNUSPDASLFDAVYSLIKHKIHRLPVIDPISGNA
LYFLTHKRILKFLQLFMSDMPKPAFMKQNLDELGIGTYHNLAFIHPDTPIIKALNIFV
ERRISALFVVDESGKVVDIYSKEDVINLABEKTYNNLDITVTQALQHBSQYFEGVVKC
SKLETLETIVDRIVRAEVHRLVVVNEADSIVGIISLSDILQALILTPAGAKQKETETE
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/organism-"Mus musculus"
/db_xref-"taxon:10090"
/clone-"MGC:18882 IMAGE:4238045"
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/protein_id="AAH15283.1"
/db_xref="GI:15929720"
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/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B"
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Compugen Ltd
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B1344527 373008 MA
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AL248229 Tetraodon
BG919314 602817782
BJ0772114 BM48865 zpm2n.pk0
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AJ395115 AJ395115
AJ396118 AJ396118
AJ396118 AJ396118
AV603335 AV603357
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AA578219 n156h03.s
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ALIGNMENTS

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RESULT 1
BI344527
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Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI344527 572 bp mRNA linear 373008 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence. BI344527 BI344527.1 GI:15037807 EST.
                                                                                                                                                                                                                                                                           Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Email: smithdemail.marc.usda.gov
Email: smithdemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. vector identified by cross_match with the -minscore 18
and minmatch 12 options.
                                                                                                                                                                                                               PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                     Plate: 119 row: I column: 11 Seq primer: ATTTAGGTGACACTATAG.
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                                       /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/note="Vector:
                  /lab_host-"DH10B"
                                                                                                                                                   Location/Qualifiers
pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
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Sus.
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Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. washU-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota: Metazoa: Chordata:
Mammalia: Eutheria: Primates:
                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA178898 413 bp mRNA linear EST 09-MAR-
zp38d10.r1 Stratagene muscle 37209 Homo sapiens cDNA clone
IMAGE:611731 5' similar to SW:AAKC_RAT P80385 5'-AMP-ACTIVATED
PROTEIN KINASE, GAMMA CHAIN ;, mRNA sequence.
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314 286 1810
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      /lab_host="SOLR (kanamycin resistant)"
/note="Organ: skeletal muscle; Vector: pBluescript SK.
/note="Organ: skeletal muscle; Vector: pBluescript SK.
/note="Organ: skeletal muscle unidirectionally.
/primer: Oligo dT. Skeletal muscle from patient with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D
                                                                                                                                  /dev_stage~"adult"
                                                                                                                                           /clone_lib="Stratagene muscle 937209"
/tissue_type="muscle"
                                                                                                                                                                                            /db_xref="GDB:4643570"
/db_xref="taxon:9606"
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                                                                                                                                                                             /clone="IMAGE:611731"
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.9e-22;
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                                                                                                                                                                                                                                                                                                               Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part o scale clone-end sequencing project of the Tetraodon nigrov genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1042)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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1 (bases 1 to 1042)
Roest-Crollius, H., J
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleost
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weissenbach,J.
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033L13 of
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Similarity 97.3%;
44; Conservative
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                                                                                                                                                                                242
                                                                         Conservative
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                                                                                                                                                         /clone_lib="g"
/clone_lib="g"
/note="Genoscope sequence ID : C0BG033CF07LP1-end : T7"
/note="Genoscope sequence ID : C0BG033CF07LP1-end : T7"
/ 282 c 241 g 271 t 6 others
                                                                                                                                                                                                                             /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="033L13"
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library G from Tetraodon nigroviridis, genomic survey
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Pred. No. 2.1e-15;
0; Mismatches 192
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nce T7 end of clone
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Neoteleostei;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
Plate: LLAM10895 row: d column: 22
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National Institutes of Health, Mammalian
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Location/Qualifiers
/note=*Organ: mammary: Vector: pcMV-SPORT6; Site_1: Sa. Site_2: NotI; Cloned unidirectionally. Primer: Oligo of Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH*
a 292 c 238 g 159 t
                                                                     /db_xref="taxon:10090"
/clone="IMAGE:4946661"
/clone=lib="NCI_CGAP_Mam6"
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/dev_stage="5 months"
/lab_host="DH10B"
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/strain="FVB/N"
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                                                                                                                                                                   National Institute of Genetics
1111 Tata, Mishima, Shizuoka 4
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                      Unpublished (2001)
Contact: Tadasu Sh
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BJ072114 NIBB Mochii normalized Xenopus tailbud
                                                                                                                                                                                                                                    Center For Genetic Resource Information
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BJ072114.1 GI:17502303
EST.
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                                                                                                                                                tshini@genes.nig.ac
                                                     /organism="Xenopus laevis"
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/clone="XL096j16"
                                                                                                                   Location/Qualifiers
/tissue_type="whole embryo"
                                  /clone_lib="NIBB Mochii normalized
                                                                                                                                                                                                                                                                                                                                                                                 Metazoa; Chordata; Craniata; Vej
Batrachia; Anura; Mesobatrachia;
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to 633)
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                                                                                                                                                                                                  411-8540, Japan
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
Phasianinae; Gallus.
1 (bases 1 to 536)
Cogburn, L.A. and Monsonego-Ornan, E.
Cogburn, L.A. and Monsonego-Ornan, E.
ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                            302-831-2822
                                                                                                                                                                                                                                                                                                                                                        cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
                           /note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
                                                                                                                                                                                             /clone="pgm2n.pk008.g21"
/clone=11b="Normalized Chicken Breast Muscle, Leg
and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
                                                                                                                                                                  /tissue_type="Breast muscle, leg muscle and
growth plate"
                                                                                                                                                                                                                                                                                       /strain="Commercial broiler and Strains 90 & 21"
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/lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                                                     /db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                      /organism="Gallus gallus"
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162 c 148 g
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Pred. No. 7.4e-08
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Cogburn, L.A. and Monsonego-Ornan, E.
ESTs from Normalized Chicken Breast Muscle, Leg Muscle,
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal
                                                                                                                                                                                                                                                                                                                                                                                                                                             Townsend Hall, Ne
Tel: 302-831-1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Larry A. Cogburn
University of Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM487789 BNA97789 BNA9 linear EST 07-FEB-2002 pgm2n.pk005.j24 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk005.j24 5' similar to gb[AAC52580.1 (U42413) '-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus
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Location/Qualifiers
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                                     /dev_stage="Breast,leg:Embryo(d19);post-hatch(ld,1,3,5,7,9,1) weeks);growth plate(ld,7d,14d post-hatch)"
/lab_host="E. coli EMOHIOB"
/note="Vector: pcMySPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing
                                                                                                                                                                              /tissue_type="Breast muscle,
growth plate"
                                                                                                                                                                                                                and Epiphyseal Growth Plate /sex="Male and Female"
                                                                                                                                                                                                                 /db_xret="-toAvu..., j24"
/clone="pgm2n.pk005.j24"
/clone_lib="Normalized Chicken Breast Muscle, Le
/clone_lib="Normalized Chicken Breast Muscle, Le
                                                                                                                                                                                                                                                                                                            /strain="Commercial broiler
Strains 90 & 21"
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                                                                                                                                                                                                                                                                                                                                               organism="Gallus
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Pred. No. 8.4e-08
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Query Match
Best Local Similarity 69.4
Matches 109; Conservative

4.78;

Score 80.2; DB Pred. No. 2e-07;

DB 10;

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Best Local Similarity
Matches 109; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717,
Tel: 302 831-1345
Fax: 302-831-3411
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BG7116. pk008.c13 Normalized Liver Library Gallus gallus cDNA clone pglln. pk008.c13 S similar to gil4506061 ref[NP_002724.1] protein kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1; Protein kinase, AMP-activated, noncatalytic, gemma-1 [Homo sapiens] gil127373489 ref[XP_006778.2] protein kinase, AMP-activated, gamma 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burnside, J., Morgan, R.W. and Cogburn, L.A. Chicken ESTs from a normalized liver library Unpublished (2001)
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                                                                                                                                                                                                                                                                 129
                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                              /tissue_type="liver"
/lab_host="E.coli EMDH10B"
/note="Vector: pCMVSPORT 6'
215 c 167 g 119 i
                                                                                                                                                                                                                                                                                                                  /organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pglln.pk008.cl3"
/clone_lib="Normalized Liver
/sex="Male and Female"
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Pred. No. 2.1e-07;
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EST.
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BM440762
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Townsend Hall, Newark, DE 19717,
Tel: 302-831-1335
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Contact: Larry A.
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ESTs from Normalized Chicken Reproductive Tract cDNA library-
University of Delaware and INRA, Tours-Poultry Unit Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: pCMVSPORT6; Library made from three total RNA pools from each tissue (testis 25%, overy 25%, and oviduct 50% of final RNA pool); Single pass sequencing from 5'-end"

a 222 c 160 g 128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Testis, ovary and oviduct"
/dev_stage="Various stages;embryonic, post-hatch, immature
and sexually-mature"
/lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Library (pgrln)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="pgrln.pk002.19"
/clone_lib="Normalized Chicken Reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Commercial broiler
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Gallus gallus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 80.2; DB 10;
Pred. No. 2.1e-07;
0; Mismatches 48;
                                                                                     649 bp
                                                                CDNA
                                                                                     mRNA
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                                                                mRNA linear
clone 21c2r1,
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SOURCE
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                                                                                                                        MEDLINE
                                                                                                                                     JOURNAL
                                                                                                                                                                                           AUTHORS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 69.4 hes 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           9CtCaagttCCtgCaCatCtttgtaagcCtgggcCca 1384
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                                                                                                                                                                    chicken.
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus
1 (bases 1 to 758)
1 (bases 1 to 758)
                                                                                                                                                                                                                                                                                                          AJ396118
AJ396118 dki
AJ396118
AJ396118.1
                       Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
                                                                                                                Abdrakhmanov,I., Lodygin,D., Geroth,P.,
J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs
analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
20568495
                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Abdrakhmanov,I., Lódygin,D., Geroth,P., Arakawa,H., Law,A., P.,J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs as a resource for the Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cellular Immunology
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                                                                                                                                                                                                                                                                                                                                      dkfz426 Gallus
∕organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9031"
/clone="21c2r1"
/clone_lib="dkfz426"
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227 c 155 g 137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gallus gallus"
/strain="CB"
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Pred. No. 2.1e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                   linear
25f16r1,
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   Query Match
Best Local Similarity
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AV603335 Bos taurus
5', mRNA sequence.
AV603335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Animal Genetics Division
Shirakawa Institute of Animal Genetics Odakura, Nishigo, Nishi-shirakawa, Fuk
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 29 (22), E108 (2001) 21570554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single pass sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Sugimoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takasuga,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV603335.1 GI:9725661 EST.
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                                                                                                                                                        144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone was obtained from a polyA-deleted cDNA library.
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                                                                                                                                     /Clone_lib="Bos taurus kidney fetus"
/clone_lib="Bos taurus kidney fetus"
/tissue_type="kidney"
/dev_stage="fetus"
/lab_host="DH10B"
/note="vector: pZL1; Site_1: Sal1; Site_note="vector: pZL1; Site_1: Sal1; Site_note="fetus"
/note="vector: pZL1; Site_1: Sal1; Site_1: Sal1; Site_note="fetus"
/note="vector: pZL1; Site_1: Sal1; Site_1: Sal
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/db_xref_"taxon:9031"
/clone_"25f16r1"
/clone_iib="dkfz426"
/tissue_type="Bursa of Fabricius"
/a 238 c 186 g 166 t
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                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="E1KI015F02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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4.48;
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Score
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76.4; DB 9;
No. 1.4e-06;
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                                                                                                                                       94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishieo, Nishi-shirakawa, Fuku
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                                      Single pass sequencing. This clone was obtained from a polyA-deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5', mRNA sequence.
AV608257
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564 bp mRNA linear EST 28-NOV-2001
AV608257 Bos taurus kidney fetus Bos taurus cDNA clone E1K1045H03
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Sugimoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                            /organisma"Bos taurus"
/db_xref="taxon:9913"
/clone="EIKI045H03"
/clone_lib="Bos taurus kidney fetus"
/tissue_type="kidney"
/dev_stage="fetus"
                                                                                                                                                                                                                   /note-"Vector: pZL1; Site_1: Sal1; Site_2: was deleted from a Not1 site" 145 c 121 g 155 t 1 others
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AA558845
448 bp mRNA linear EST 09-SEP-1997 n169b09.sl NCI_CGAP_Pr4.l Homo sapiens cDNA clone IMAGE:1045913 similar to SW:AAKG_RAT P80385 5'-AMP-ACTIVATED PROTEIN KINASE,
                                                                                                                                                                                                                                                                                                                                                                                           98;
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Plate: LLAM11569 row: a column: 13
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Tissue Procurement: Life Technologies,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:5226132"
/clone_lib="NIH_MGC_120"
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/db_xref="taxon:9606"
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Best Local Similarity 68.1%;
Matches 98; Conservative
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 561 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 297.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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//lab_host-"DH10B"

//note-*Organ: prostate; Vector: pAMP10; mRNA made from prostatic intrapplithelial neoplasia (high-grade), cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research b. Si:5380-5383. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Homo sapiens"
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grade"
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ALIGNMENTS

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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                       Sequence 3 from Patent WO0177305. AX381580
                                                                                  Andersson,L., Luthman,H. and Marklund,S. Variants of the human amp-activated protein kinase gamma 3 subunit Patent: WO 0177305-A 3 18-OCT-2001; Arexis AB (SE)
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Homo sapiens
clone
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Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32

ACCESSION

ACC27416.2

GI:8317289

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ACC27416

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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lamazarcs, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., O'Liver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stantos, R., Schauer, S., Severy, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 135376 bases at least 040 Consensus quality: 135376 bases at least 030 Consensus quality: 146503 bases at least 020 Insert size: 161000; agarose-fp Insert size: 149029; sum-of-contigs Ouality coverage: 3.1 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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7548 7647: gap of 100 bp
7648 9983: contig of 2336 bp in 1
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143: gap of 100 bp
17123: contig of 100 bp
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21928: contig of 2362 bp in length
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66595: gap of 100 bp
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73218: contig of 5523 bp in length
73219
73318: gap of 100 bp
77215: contig of 3797 bp in length
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77216
85022: contig of 7807 bp in length
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85122: gap of 100 bp
85123
93314: contig of 8192 bp in length
93315
93414: gap of 100 bp
101193: contig of 7779 bp in length
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101294
101399: contig of 11797 bp in length
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113190: gap of 100 bp
113190: gap of 100 bp
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123596: gap of 100 bp
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27059: contig of 2640 bp in length
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                                                                                                                                                                                                                                                                                                                                                  Score 1719.4;
Pred. No. 0;
0; Mismatches
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1680	catcctgactgcactggacatctttgtggaccggcgtgtgtctgccactgcctgtggtcaa	1621	Qy
1620 34999	Latccaagaltigggcatcggcacattccgagacttggctgtggtgctggagacagcacc	35058	Db VY
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o d		11	Db 1
Λ.	ctqqtcccatcctaaccaaqqttccctqctqcccaaccctccttcct	1501	O _V
		\vdash	Db
1500	cctagcagtcgtggggaagagctgggagccctcttgaagctgctgggatccctgatctc	1441	Qy
35179	CCCAGGTGGGAGGAGAGCCTGGGCAGGTGATCAGAGGGCCTGAGGAGTCTTCAG	35238	Db
1440	ccaggtgggaggaagggggagacctgggcaggtgatcagagggcctgaggagtcttc	1381	Qy
35239	ACTCCACATCCTCACACACACACGCCTGCTCAAGTTCCTGCACATCTTTGTAAGCCTGGG	35298	рь
1380	ctccacatcctcacacacaaacgcctgctcaagttcctgcacatctttgtaagcctgg	1321	Qy
35299	CACCCTCATCAAGAACCGGATCCATCGCCTGCCTGCTCTTGACCCGGTGTCACGCCAACGT	35358	Db
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35359	CTCCCTAGGCTGCCCCGAGGCTCACTGCTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTA	35418	Db
1260	tocotaggotgococgaggotoactgctcocatototgcagcotgtttgaagctgto	1201	Qy
35419	CAGACAAGGGAGCCTTGGTGCCCTGCCCTTTTTTAGGGGCCTGGGATGGAGGTTGTCT	35478	Db
1200	agacaagggagccttggtgccctgccctcctttttaggggcctgggatggaggttgtc	1141	Qy
35479	ACAGTCCCCTTCCCCAGTCCCACTCAGCTCTGAACTCACCTCTTCATCCTAGGCGCACA	35538	Дb
1140	cagicocoticoccagicocacicagototgaacicacototicatoctaggoggoac	1081	Qy
35539	CTCCATCTCTCCTAATGGTGGGTGTCTCTGCTCATTCACCTGAGCCTCCTCCTCCCC	35598	DЬ
1080	tocatototoctaatgataggtgggtgtototgctcattcacotgagcotcotcotco	1021	Qy
35599		35658	Db
1020	ggcctgactctggctctttctgcagagatctacctgcaaggctgcttcaagcctctgg	961	Qy
35659	GGTGCCTGACGGAAGGGAAGCTGCCTGGGACTGCAAGGTGACGCAGGTGACCGGCTCCCC	35718	Db
960	tycctyacygaayygaayctycctyyyaactycaaygtyayycagytyaccygctccc	901	Оу
35719	GTGGAGGATGGGCAGTGGGGATGTCCTGGAGTGAACAGGGGAGGGA	35778	Дb
900	tggaggatgggcagtggggatgtcctggagtgaacaggggaggga	841	Qy
35779	GGGTGAGTGGGGAGAGGAACCCGGAAAGGGGCTGTTGGTGATGGTGGGCCAGGGCTTAAG	35838	Db
840	ggtgagtgggggagaggaacccggaaaggggctgttggtgatggtgggccagggcttaa	781	ОУ
35839	CTGTCGATGTCTCTAGGTCCAGATCTATGAGATTGAACAACATAAGATTGAGACCTGGAG	35898	Дb
780	tgtcgatgtctctaggtccagatctatgagattgaacaacataagattgagacctgga	721	Qy
35899	AGGGGAGTCCTCCTGGAGCCTGGTGCCCCTAGAAGCCCACGTCTTTCTGACTTCTGGAGTC	35958	DЬ
720	ggggagtcctcctggagcctggtgccctagaagcccacgtctttctgacttctggagt	661	Оу
35959		36018	Дb
660	gtccccctggtgaggagtgggctgggaatcttatgggcacccagagggggggg	601	Ωу
ō .		7	Db
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VERSION KEYWORDS SOURCE

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JOURNAL

TITLE JOURNAL AUTHORS

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AUTHORS
TITLE
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Sequencing vector: M13; 98%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 98% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 187795 bases at least Q40
Consensus quality: 190513 bases at least Q30
Consensus quality: 192099 bases at least Q20
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On Feb 21
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Waterston,R.H.
Direct Submission
Submitted (08-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 5.58 in Q20 bases; agarose-fp Quality coverage: 5.67 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Sequencing Center Center code: WUGSC
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17 unordered pieces.
ACO73128
                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 200000; agarose-fp
Insert size: 194954; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: H_NH0647005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                   as soon as it is available and the accession number will be preserved.
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                      1157: contig o

1257: gap of u

3600: contig o

3700: gap of u

5103: contig c

5203: gap of u

8524: contig c

8624: gap of u

11856: contig c

11856: contig c

11956: gap of u
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/db_xref="taxon:9606"
/chromosome="2"
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/note-"assembly_name:Cont1932"
149388 196554
/note-"assembly_name:Cont1933
clone_end:SP6
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44743, 58275
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3701. .5103
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130426. .149287
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15884. .21906
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73816: contig of 15441 bp in 16
73916: gap of unknown length
73916: gap of unknown length
92140: contig of 18224 bp in 16
92240: gap of unknown length
113337: contig of 21097 bp in 16
113437: gap of unknown length
130425: contig of 16888 bp in 16
130425: gap of unknown length
149287: contig of 18862 bp in 16
149287: gap of unknown length
149287: gap of unknown length
149287: contig of 47167 bp in 16
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                CTCCATCTCCCTAATGATAGGTGGGTGTCTCTCCTCATCACCTGAGCCTCCTCCTCCCCC
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Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
99067792
                                                                                       The sequence of Homo sapiens Unpublished (2001)
                                     Waterston,R.H.
Direct Submission
Submitted (08-SEP-1999) Genome
University School of Medicine,
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Waterston,R.H.
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Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Nov 8, 2001 this sequence version replaced gi:13431203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                         Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 AC009974. A single plasmid region exists beteen 38812-38903. unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.
                                                                                                                                                                                                                                                                                                                The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-647O5. Actual start of this clone is at base position 1 of RP11-459I19; actual end is at base position 206854 of RP11-459I19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. 1 MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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------ Summary Statistics
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                                         cctcccctgcagggatgctgaccatcactgacttcatcctggtgctgcatcgctactaca
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Submitted (10-DEC-1999) Dept Animal Breeding and Genetics,
University of Agricultural Sciences, BMC Box 597, Uppsala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 5888)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gallin,J., Lundstrom,K.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.I
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HEMQEHTCYDAMATSKLVIFDTMLEIKKAFFALVANGVAPADUNDSKQSFVQALTI
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KNRIHRLPVLDFVGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
AVVLETAPILTALDIFVDRKYSALPVNETGQVVGLYSRFDVIHAAQQTYNHLDMNV
GENIGORFILITALDIFVDRKYSALPVNETGGVVGLYSRFDVIHAAQQTYNHLDMNV
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Join(1. 154,515. 918,1809. 1890,2349. .2407,2509.

2771. .2825,3027. .3153,3286. .3451,4578. .4615,4791.

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Direct Submission
Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular Blotechnology, Beutenberstr. 11, Jena 07745, Germany
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Sequence
AX281582
                    Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                       AX281582.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57663
             (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.2%;
milarity 67.6%;
Conservative
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17870
17970
32747
32847
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/db_xref="taxon:10090"
/chromosome="1"
/clone="pac510; pac457"
a 55423 c 56238 g 58199
                                                                                                               5
                                                                                                                                                                                                                                                                                                                                               -CTAGATCAAGTGTCTTGATCTGATGAGATCACTACCATGTCCCATCCTA
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1. .227724
                                                                                                                 from
                                                                                       GI:16608833
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17969: gap of unknown Length
32746: contig of 14777 bp in 1
32846: gap of unknown Length
227724: contig of 194878 bp in
Luthman, H.
                                                                                                               1647 bp
Patent WO0177305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 209.4; DB 2;
Pred. No. 2.3e-40;
0; Mismatches 126;
and
Marklund,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58199
                        Craniata; Vertebrata;
Catarrhini; Hominidae,
                                                                                                                            DNA
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                                    Euteleostomi;
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SOURCE
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Best Local S
Matches 173
                                                                                                                                                 TITLE
                                                                                                                                                                                          AUTHORS
                                                                                                                        JOURNAL
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                                                                                                                                                                                                                                                                                               Ax099776
Sequence 3
Ax099776
                                                                                                                                                                                                                                                                                                                                                                                             1189
                                                                                        same, and uses thereof
Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2109)
                                                                                                                                              Variants of the gamma chain of ampk,
                                                                                                                                                                      Andersson,L., Looft,C., Kalm,E., Milan,D., Rol
Rogel-Gaillard,C., Tannuccelli,N., Gellin,J.,
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                     AX099776.1
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Patent: V
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GSLLPRDSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGOV
VGLYSRFDVIHLAAQOTVNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIARE
QVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDALGA*

502 c 462 g 337 t
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SSERIKGKRRAKALRWTRQKSVEEGEPFQGEGFRSRPAAESTGLEATFPKTTPLAQA
DPAGVCTPPTCWDCLFSBCTASAGSSTDDVELATEFRTEAMECELEGLLEERPALC
LSPQAPFPKLGWDDELRKPGAQIYMRFWGEHTCYDAMATSSKLVIFDTMLEIKKARFA
LVANOVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIGHKIETWREIY
/note="unnamed protein product"
/codon_start=1
                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                             Location/Qualifiers
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20. .1489
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/db_xref="GI:16608834"
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l. .1647
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from Patent W00120003.
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Pred. No. 4.2e-30;
0; Mismatches 8
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Ernst (DE)
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Best Local
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Sequence
AX099802
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tttgggcatcggcacattccgagacttggctgtggtgctggagacagcacccatcctgac 1629
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          same, and uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variants of the gamma chain of ampk, dna sequences encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                          /translation="MSFLEQENSSSWPSPAYTSSSERIRGKRRAKALRWTRQKSYEEG
EPPGGGEGPRSRPTAESTGLEATFPKTTPLAQADPAGYGTPTGWDCLPSDCTASAAG
SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
RFWGEHTCYDAMATSKLVIFDTMLEIKAFFALVANGVAPAPLWDSKQSFYGMLTI
TDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSKFEAVYTLI
KNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL
AVVLETAPILTALDIFYDRRYSALPYVNECGQVYGLYSRFDVIHLAAQQTYNHLDMSV
GEALRORTLCLEGVLSCOPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA"
                                                                                                                                                                                                                               /codon_start=1
/protein_id="CAC35801.1"
/db_xref="GI:13538837"
                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
1. .1395
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HLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDE
TQHLLGVVSLSDILQALVLSPAGIDALGA*
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/db_xref="G:13538811"
/db_xref="G:13538811"
/translation="mremgehtcydawatssklviedtwleikkaffalvangvraap
LWDSKKQSFVUMLTITDFILVLHRYYRSPLVQIYEIEOHKIETWREIYLQGCFKPLVS
LSPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFL
                                                                                                                                                                                                                                                                                                       /note="unnamed protein product"
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Ernst (DE)
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REFERENCE
AUTHORS
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AUTHORS
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Matches 173; Conserv
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Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A.,

Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N.,

Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.

Direct Submission

Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 2115)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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AF214519
AF214519.1 GI:8215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 288 (5469), 1248-1251 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    skeletal muscle
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           /codon_start=1
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SSTDDVELATEFPATEAWECELEGILEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
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                                                                                                                                                                                               /tissue_type="skeletal muscle"
1. .2115
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                         /gene="PRKAG3"
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gamma subunit (PRKAG3)
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CDS

/gene-*AMPK gamma 22. .1500

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/organism="Homo sapiens" /db_xref="taxon:9606"

/translation="MEPGLEHALRRIPSWSSLGGSEHQEMSFLEQENSSSWPSDAVTS SSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEATFPKTTPLAQA DPAGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALC LSPQAPFPKLGWDDELRKPGAQIYMRFIEEHTCYDAWATSSKLVIFDTMLEIKKAFFA

/evidence=experimental /product="AMP-activated /protein_id="CAB65117.1" /db_xref="GI:6688201"

ed protein kinase

gamma

3 subunit*

subunit'

/gene-"AMPK gamma 3" /function="AMP-activated

protein

kinase

/codon_start-1

gene

source

London,

W12 ONN, UNITED KINGDOM Location/Qualifiers

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Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding Blochem. J. 346 Pt 3, 659-669 (2000)
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  Submitted (12-OCT-1999) Carling D., Ce Clinical Sciences Centre, Hammersmith
                                        Carling, D
                             Direct Submission
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                              (AMPK gamma 3 gene).
AJ249977
                                                                                                                                                                                                                                                       Homo sapiens mRNA for AMP-activated
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KNRIHRLPYLDPYSGNYLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL
AVYLETAPILTALDIFYDRRYSALPYVNECGQVYGLYSRFDYIHLAAQQTYNHLDMSY
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Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pig.
Sus scrofa
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Mammalia;
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                                                                                    /translation-"MHEMQEHTCYDAMATSSKLVIEDTMLEIKKAFFALVANGVRAAP LWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVS ISPNDSLFEAVYALIKNRIHRLFVLDFVSGAVLHILTHKRLIKFLHFGTLLBRPSFL YRTIODLGIGTFRDLAVVLETAPILITALDIF VDRRVSALPVNETGQVVGLYSRFDVI HLAAQQTYNHLDMNVGEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDE TQHLLGVVSLSDILQALVLSPAGIDALGA"

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                                                                                                                                                                                                                                                               /organism="Sus scrofa"
/db_xref="taxon:9823"
472. .1389
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LQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIF
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VGLYSRPDVHILAQQTYNHLDMSVGEALRKRTLCLEGVLSCQPHESLGEVIDRIARE
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a 674 c 617 g 498 t
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                                                                                                                                                                                                                                             /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .1867
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O; Mismatches
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1 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1873)
Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A.,
Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K.,
Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                      /codon_start-1
/product="awp-activated protein kinase gamma subunit"
/protein_id="akp73988.1"
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/db_xref="GI:8215684"
/db_xref="GI:8215684"
/db_xref="GI:8215684"
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/dc_xref="GI:821684"
/dc_xref="GI:82
                        GEALRORTLCLEGVLSCOPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA"
1 580 c 535 g 376 t
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l. .1873
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/map="15q"
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/db_xref="taxon:9823"
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(PRKAG3)
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Sus scrofa
Eukaryota;
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160; Conserv
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Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT MAPIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
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Sequence 27 from Patent
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/db_xref="G:13538835"
/db_xref="G:13538835"
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HFMGEHTCYDAMATSKLVIFDTMLEIKKAFFALVANGVRAAPLDSKKQSFGMLTI
TDFILVLHRYYRS9LVQ1YEIEEHKIEFWREIYLQGCFKPLVSISPRDSLFEAVYALI
KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
AVVLETAPILTALDIFVDRVSALPVVNETGQVVGLYSRFDVHLAAQQTYNHILDMNV
GEALRQRTLCLEGVLSCQPHETLGEV IDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA"
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                                                                                                                                                                                                                                                                                                                                                                                         /note="unnamed protein product"
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/db_xref="taxon:9823"
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Eutheria; Cetartiodactyla; Suina; Suidae;
1 to 1873)
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patent: WO 0120003-A 31 22-MAR-2001;
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Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
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Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Tannuccelli, N., Gellin, J., le Roy
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Human immune/haema

Human AMP-activate PRKAG3 cDNA. Homo Human AMPK gamma Human AMPK gamma

Human colon cancer
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RESULT 2
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                            discase;
                                                                                                                                                                                                                   Human; microarray;
                                                                                                                                                                                                                                      Human
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                                                                                                                                                                                                                                     breast cell single exon nucleic acid
                                           MOLECULAR DYNAMICS
                                                                                                                                                                                                            cancer;
                                                           2000US-0180312
2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0236359
2000US-0236359
                                                                                                                                     2001WO-US00662
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                         Rank
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The invention relates to a spatially-addressable set of single exon CC nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting CC from human breast and BT 474 cells. The method involves contacting CC the probes with a collection of detectably labelled nucleic acids could to each probe of the microarray. The probes are useful for CC verifying the expression of regions of genomic DNA predicted to cencode proteins. They are useful for gene discovery, and for CC determining predisposition and/or prognosing breast disease. Gene CC expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater CC diversity of probes for measuring gene expression, with far less bias CC than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. CC Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly considered the production int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for measuring gene expression in breast, comprises number of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spatially-addressable set of single exon nucleic acid probes, ful for measuring gene expression in sample derived from human ast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID NO 3401;
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Sequence

378

BP;

80

A; 128

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97

ç; 73 T;

0 other;

20.48;

Length

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RESULT 3
ABA55162/c
ID ABA55162 standard; DNA; 3
XX
AC ABA55162;
XX
DT 01-FEB-2002 (first entry
XX
DT 01-FEB-2002 liver single
XX
KW Human foetal liver; gene
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362; Conservative
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Pred. No. 6.9e-83;
D; Mismatches 0
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liver single exon

nucleic acid probe

gene

expression;

single

exon

nucleic #3467.

acid

probe;

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entry

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03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
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                                cctggcccctcagatcaagaaggccttctttgctctggtggccaacggtgtgcgggcagc
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                                                                              99agtctgcatggccagctgggagaccctggggctcaatttccccatctgtggagccgct
                                                                                                                   accacaagcttggcttcaggccaagcccagccaggggccagggtggaggaaagtccatcc
                                                                                                                                                                                   CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGTGAGGAGAGGCTGGGGAGGTGAAG
                                                                                                                                                                                             ccctctatgggacagcaagaagcagagctttgtgggtgaggagaggctgggggaggtgaag
                                                                                                          ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGCGAGGGGCCAGGGTGGAAGGTCCATCC
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2000US-0207456
2000US-0608408
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2000US-0236559
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2000US-0236559
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Pred. No. 6.9e-83;
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                                                                                                                                                                                                                                                                                                             T; 0
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ABA24907/c
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Best Local
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                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systems. Congenital heart disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
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                                                                                                                                                                                                                                                                                                                                                           Single
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                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-)
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cardiovascular disease;
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                                                                              cctggcccctcagatcaagaaggccttctttgctctggtggccaacggtgtgcggggcagc
           99agatggaggaggtgagggggggagatcttgtacggttgttctggggctgatctctgatat
GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT
                                       CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGTGAGGAGAGGCTGGGGAGGTGAAG
                                                    2001-488899/53
                                                                                                                        al Similarity 99.7
362; Conservative
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-06323687.
2000US-0234687.
2000US-0234687.
2000US-0236359.
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hypertension; cardiac
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RESULIT 5
AAKO34
XX AAKO34
AC AAKO34
XX DT 05-NOV
XX Human
XX Human
XX Human
XX Human
XX Homo s
XX WO2001
XX WO1-PE
PR 20-SEP
PR 27-SEP

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brains
                                                                                                                                       probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        cervical cancer;
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probes of the
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                                                                             MOLECULAR DYNAMICS INC
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Query Match
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Matches 362; Conserv
                                                                                                                                                                                                               The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                           Sequence 378 BP; 80 A; 128 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells
         Conservative
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                                20.4%;
         0;
   Score 351; DB 22;
Pred. No. 6.9e-83;
D; Mismatches 0
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                      agc
                                              atgaccagctgacacctttcacctccgctactgcatggccctgtgccataggtgctaggg
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RESULT 8
AAI34821/c
                                       Homo
                                                         Probe; microarray; human;
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                          WO200157272-A2
                                                    genetic
                                                                         Probe #3507
                                                                                     17-OCT-2001
                                                                                                                AAI34821 standard; DNA; 378
                                                    disorder;
                                                                        used
                                                                                    (first entry)
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                                                                       measure gene expression in human placenta sample.
                                                         placenta;
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diagnosis,

30-JAN-2001; 2001WO-US00663

09-AUG-2001.

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RESULT 9
AA103344/c
ID AA103344 standard; D
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AC AA103344;
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DE Probe #3335 used to
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KW Probe; human; breast
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                  Probe #3335 used to
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes The present sequence is one surbe. The probes are useful for producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                  The present invention relates to novel single exon nucleic acid in the present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where i hybridises at high stringency to a nucleic acid expressed in the breast. The probes are useful for predicting, diagnosing, grading staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The disease include: breast cancer, disorders of development, inflammatory diof the breast, fibrocystic changes, proliferative breast disease mon-carcinoma tumours.
                                Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wlpo.int/pub/published_pct_sequences.
 Sequence
                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                                                                                Novel single
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-)
                                                                                                                                                                                                                                                                                                                a human
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                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS
   378
                                                                                                                                                                                                                                                                              SEQ
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                                                                                                                                                                                                                                                                                                              le exon nucleic
breast -
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-02346359.
 ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001WO-US00661
                                                                                                                                                                                                                                                                              ID No
 80
A; 128
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                                                                                                                                                                                                                                                                                                                                                                                                     Chen
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                                                                                                                                                                                                                                                                                                                                acid
                                                                                                                                                                                                                                                                            322pp;
 C;
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 97
                                                                                                                                                                                                                                                                                                                                                                                                     Rank
                                                                                                                                                                                                                                                                                                                                probe
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                                                                                                                                                                                                                                                                              English
 73
                                                                                                                                                                                                                                                                                                                                                                                                     DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      breast disease;
                                                                                                                                                                                                                                                                                                                                used
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 other;
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                                                  part of the printed directly from WIPO
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lammatory diseases
ast disease and
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                                                                                                                                                                   grading,
                                                                                                                                                                                                                                                                                                                                expression
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Query Match
Best Local S
Matches 362
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     62
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cctggcccctcagatcaagaaggccttctttgctctggtggccaacggtgtgcgggcagc
                                                               ggagtctgcatggccagctgggagacccttgggggctcaatttccccatctgtggagccgct
                                                                                                                    accacaagcttggcttcaggccaagcccagccaggggccaggggtggaggaaagtccatcc
                                                                                                                                                                          ggagatggaggaggtgagggggagatcttgtacggttgttctgggggctgatctctgatat 180
                                                                                                                                                                                                                           ccctctatgggacagcaagaagcagagctttgtgggtgaggagaggctggggaggtgaag
                                                                                                        ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGCCAGGGCCAGGGTGGAGGAAAGTCCATCC
                                                                                                                                                           GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT
                                                                                                                                                                                                               CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGTGAGGAGGGCTGGGGAGGTGAAG
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                   Score 351; DB Pred. No. 6.9e 0; Mismatches
                                                                                                                                                                                                                                                                                                                      0;
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                                                                              300
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Q 멍 Q

В δ

Local Similarity

20.4%;

DB 22; .9e-83;

Length

378;

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В Qy DЬ Ş

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361

agc 363

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CC sequences ABA08235-ABA09574 represent nucleic acids encoding them. The CC invention also relates to vectors and recombinant host cells comprising a CC nucleotide of the invention, methods of producing the novel polypeptides, cc or polypeptides against the polypeptides, methods of detecting the nucleotides CC or polypeptides in a sample, and methods of identifying compounds which CC bind to polypeptides of the invention. Although novel, many of the CC polypeptides of the invention have homology to known proteins, thereby CC glving an insight into their probable biological activities, and hence CC polypeptides activities, including cytokine, cell proliferation or cell therapeutic applications. The polypeptides of the invention may CC have various activities, including cytokine, cell proliferation or cell chaematopolesis regulatory activity; tissue growth factor activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be considered in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antificanti; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; growth for haematopolesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; myeloid cell disorder; lymphold cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                             Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arthritis
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)B; ABB11241.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
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                                                                                                                                                                                                                                                                                                                                                              ABB10981-ABB12330 represent 1350 novel human polypeptides, ABA08225-ABA09574 represent nucleic acids encoding them. T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cc conditions, e.g., by protein or gene therapy. Such conditions include cc cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cd disorders), chronic inflammatory conditions (e.g., asthma or arthritis), cc disorders), chronic inflammatory conditions (e.g., asthma or arthritis), cc arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal cc vascular growth. Polypeptides involved with tissue regeneration and cc repair (or nucleic acids encoding them) may be used to promote wound cc healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, cc bacterial and fungal infections in addition to immune disorders. Cc Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to promote cells danaged by illness, can be used to augment or replace cells danaged by illness, can anipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells danaged by illness, can anipulate stem cells in the diagnosis of the above conditions, and in drug covered in the diagnosis of the above conditions, and in drug covered in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 202;
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Best Local
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                                                                                                                                                                                                                                                                 Human; AMP-activate
metabolic disease;
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                                         variation
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                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                           PRKAG3 cDNA
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                                                                                                                                                                                                                                                                                                                                                                 AAH43685;
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                                                                                                                                                                                                                                      sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               tacccaccccaagatgagaggctcgggctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tgcactggacatctttgtggaccggcgtgtgtctgcactggctgtggtcaacgaatgtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMP-activated protein kinase gamma 3 subunit; PRKAG3; lic disease; diabetes; obesity; substitution; ss.
                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                                                                                                                                                                                                                                                                    (first
                                                                                             /note=
559
                                                                                                                                                                                           Location/Qualifiers 20..1489
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                                                                                                                                                                                                                                                                                                                                    entry)
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95.3%;
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"C230G"
d
"C1037T"
                                                   "Silent variation"
                                                                                                         "Causes P71A"
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                                                                  "T559C"
                                                                                                                                                                 "PRKAG3"
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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No. 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
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RESULT 1
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Best Local
                                                                                                                                                                                                     1690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3,4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution PTA; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1337, resulting in the amino acid substitution RA40W. There may also be variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.
    Human; gamma
                       Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA
                                                                                                                                                                             1189
                                                                                                                                                                                                                               1129
                                                       13-JUN-2001
                                                                                   AAD03296;
                                                                                                                                                                                                                                                                                   1069
                                                                                                           AAD03296 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-657170/75.
P-PSDB; QQB47679.
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                                                                                                                                                                                                     t 1690
                                                                                                                                                                                                                       tgcactggacatctttgtggaccggcgtgtgtctgcactgcctgtggtcaacgaatgtgg
                                                                                                                                                                                                                                      tgcactggacatctttgtggaccggcgtgtgtctgcactgcctgtggtcaacgaatgtgg
                                                                                                                                                                                                                                                                         tttgggcatcggcacattccgagacttggctgtggtgctggagacagcacccatcctgac
                                                                                                                                                                                                                                                                                                                                                                                        173;
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                   9.8%;
nilarity 95.6%;
Conservative
subunit; adenosine monophosphate-activated kinase;
                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Causes R340W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 A; 502 C; 462 G;
                                                                                                           DNA; 2109
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                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                   Score 168.2;
Pred. No. 2.5e
0; Mismatches
                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    337
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8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   other;
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AMPK;
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δÃ B

909

Query Match Best Local Matches

Local

Similarity 95.073; Conservative

9.8%;

Score 168.2; Pred. No. 2.86 0; Mismatches

.8e-34

Indels Length

Gaps

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Sequence

2109

BP;

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621 C;

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0 other;

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CC useful as therapeutic for treating carbohydrate metabolism disorders such CC as diabetes, obesity, and disorders associated with muscle metabolism CC such as myopathy and cardiovascular diseases, to modulate AMPK CC activity, and for restoring a normal AMPK function. PRKAG3 sequence CC and its functionally altered mutants are useful for the diagnostic CC evaluation, genetic testing and prognosis of a metabolic disorder, CC preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are CC useful for detecting a dysfunction of carbohydrate metabolism resulting CC from the expression of a functionally altered allele of PRKAG3.

CC Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for Screening compounds able to modulate AMPK activity. Nucleic acid CC screening compounds able to modulate AMPK activity. Nucleic acid CC encoding PRKAG3 is useful for detecting mutations in a PrKag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain cxx
                                                                                                                                                                                                                                                                       The present sequence is a cDNA encoding human adenosine monophosphat (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle PRKAG3 is
                                                                                                                                                                                                                                                                                                                                                                                               New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INRG )
                                                                                                                                                                                                                                                                                                                                                         Claim 12; Fig
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Iannuccelli N,
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5'UTR
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18-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KALM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LOOF/)
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LOOFT C.
KALM E.
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472..1389
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Chardon P;
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AID AADO 320
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             The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
evaluation, genetic testing and prognosis of a metabolic
                                                                                                                                                                                                                                                                                      Claim 12; Page 65-68; 71pp; English
                                                                                                                                                                                                                                                                                                                                                           New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
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Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INRG ) INRA INST NAT RECH AGRONOMIQUE (ANDE/) ANDERSSON L. (LOOF/) LOOFT C.
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18-MAY-2000; 2000EP-0401388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUN-2001
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Gellin
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/product=_"Human_complete_Prkag3_protein"
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y P, Chardon
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Best Local
(INRG )
(ANDE/)
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18-MAY-2000;
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                                                                                        22-MAR-2001
                                                                                                                                                                                                                                                         PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorec genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus; chromosome 15; ss.
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                                                                                                                                                                                                                                        Sus scrofa
                                                                                                                                                                                                                                                                                                                              Pig AMPK gamma
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                                99EP-0402236
2000EP-0401388
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         NAT RECH AGRONOMIQUE
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                                                                                                                                                                                                                                                                                                  adenosine monophosphate-activated kinase;
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Pred. No. 2.1
                                                                                                                                                         scrofa
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CC Mutation in Prkag3 results in an altered regulation of carbohydrate CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as CC diabetes, obesity, and disorders associated with muscle metabolism cC such as myopathy and cardiovascular diseases, to modulate AMPK CC activity, and for restoring a normal AMPK function. PRKAG3 sequence CC and its functionally altered mutants are useful for the diagnostic CC evaluation, genetic testing and prognosis of a metabolic disorder, CC preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3 are CC useful for detecting a dysfunction of carbohydrate metabolism resulting CC from the expression of a functionally altered allele of PRKAG3. CC Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid cencoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or CC in a sequence encoding the first cystathione beta synthase (CBS) domain CC of PRKAG3 and is useful in gene therapy.
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PRKAG3;
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           cystathione beta synthase;
                    PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorec genetic testing; carbohydrate_metabolism disorder; skeletal_muscle;
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                                                                                 gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
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N, Gellin
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                                                     adenosine monophosphate-activated kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a cDNA encoding pig adenosine monophosphate (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, complete prkAG3. PrkAg3 gene is located in the RN locus of chromosome 15. Mutation in PrkAg3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as therapeutic, obesity, and disorders associated with muscle metabolism disorders.
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) LOOFT C.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 has represented the second 
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GENERAL INFORMATION:
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1018
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                            tgactctggctctttctgcagagatctacctgcaaggctgcttcaagcctctggtctcca 1025
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1800 Diagonal Road, Suite 500
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                                                                                                                                                                                                                                                                               Conservative 223;
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6.2%; F
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                                                                                                                                                                                                                                                                       Score 67.6; DB 1;
Pred. No. 1.6e-08;
23; Mismatches 152;
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                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
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APPLICANT:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
TOPOLOGY: line
IMMEDIATE SOURCE:
LIBRARY: PENIT
                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KINASES
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                                                 STRANDEDNESS:
                                                                                                                                                 TELEFAX: 415-845-4166
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CITY: Palo Alto
                                                                                 LENGTH:
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Shah, Purvi
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Corley, Neil C.
Guegler, Karl G.
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   PENITUT01
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                                                 single
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TYPE: nucleic acid
TYPEDNESS: single
TYPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PENITUTO1
LIBRARY: PENITUTO1
US-09-272-796-14
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Matches 89; Conserv
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                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1435 base pair
                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
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                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/272,796 FILING DATE:
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                       Billings, Lucy J
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                                                                                                1435 base pairs
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Corley, Neil C.
Guegler, Karl G.
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Shah, Purvi
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Pred. No. 8.8e-08;
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US-08-232-463-14 PTZgpt-F1s
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                  Query Match
Best Local s
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Best Local Similarity 67.9%;
                                                                                                                                                                       TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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   Local Similarity 3.6%; hes 13; Conservative
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                                                                                                                              STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                              NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                              FILING DATE: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
3.5%; Score 61; DB 1; Length 7218 llarity 3.6%; Pred. No. 9.6e-07; Conservative 212; Mismatches 132; Indels
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                               DB 1; Length 7218;
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Sequence 17, Application US/09007005B
Patent No. 625858
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Szostak, Jack W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT APPLICATION NUMBER: 00/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
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: LOCATION: (1)...(289)
: OTHER INFORMATION: n = A,T,C
US-09-007-005-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
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US-08-658-136-2/c
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; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C
US-09-244-796-17
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APPLICANT: ROBERTS, RICHARD W.
APPLICANT: LIU, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNJ
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 198-01-14
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US-09-244-796-17
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Best Local S
Matches 6
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SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 17
LENGTH: 289
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Patent No. 6281344
                                                                                                                                                                                             GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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  NUMBER
                    APPLICANT: QIAN, F
TITLE OF INVENTION:
                                                             APPLICANT:
                                                                                                      APPLICANT: LANDES, GREGORY APPLICANT: BURN, TIMOTHY C APPLICANT: CONNORS, TIMOTHY
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SEQUENCES:
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                                                         CONNORS, TIMOTHY D
DACKOWSKI, WILLIAM
GERMINO, GREGORY
                                         QIAN, FENG
                                                                                                                                                                    KLINGER,
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                  POLYCYSTIC KIDNEY DISEASE GENE
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2.7%; Pred. No. 0.16;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08658136 Patent No. 6071717
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Best Local
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                                                                                                                                                                     APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
                                                                                                                                                                                                                             APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TINOTHY C
                                                                                                                                        TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: PALENTIA Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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ADDRESSEE: GENZYME CORPORATION
                                                                        STREET: ONE MOUNT
CITY: FRAMINGHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: STRANDEDNESS: SIR
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REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
                                               COUNTRY:
                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/658,136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: FRAMINGHAM
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                                                                                                                                                                                                                                                                                INFORMATION:
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                                                              MASSACHUSETTS
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                                                                                                          GENZYME CORPORATION
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Floppy disk
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                                                                                                                                         POLYCYSTIC KIDNEY DISEASE GENE 58
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Pred. No. 1.7;
0; Mismatches
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US-09-165-264-7
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INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 53577 base pairs

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: Vinayaga
                                                                                                                        Matches
                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                               SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09165264 Patent No. 6197510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 52.1%; Matches 87; Conservative
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                  LENGTH: 320
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
897
                                                                  126
                                                                             777 ggaggggtgagtggggagaggaacccggaaaggggctgttggtgatggtgatgggccagggct 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       837 taaggtggaggatggggatgtggggatgtcctggagtgaacagggggaggacaataggagc 896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctcgggtgcctgacggaagggaagctgcctgggactgcaaggtgagg 943
                                                            95;
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                                                                                                                                                                                                                                                                                                                                                     Vinayagamoorthy, Thuraiayah
IVENTION: Multi-Loci Genomic Analysis
:NCE: 44747
                                                                                                                       Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                     Score 38.6; D
Pred. No. 0.27
0; Mismatches
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Query Match

2.28;

DB 4;

Length 319;

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CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 319
TYPE: DNA
ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-8
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US-09-165-264-8
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; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-14
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Patent No. 6197510
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09165264 Patent No. 6197510 GENERAL INFORMATION:
                                                                                                                                                                       APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
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                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
OKGANISM: Artificial Sequence
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RESULT 14
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; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-13
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US-09-165-264-13
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Sequence 11, Application US/09165264
Patent NO. 6197510
GEMERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 320
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                                                                                                                                                                                                                                                                                                                                                                                                             Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                    957 cccctggcctgac
                                                                                                                                                                    307 acgagggcatgcc
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Local Similarity 49.28;
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nes 92; Conserv
                                                                                                                                                                                                                                               ctcgggtgcctgacggaagggaagctgcctgggactgcaaggtgaggcaggtgaccggct 956
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Pred. No. 1.2;
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RESULT 15
US-07-959-943-6/c
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: SUPTWARE: PatentIn Ver. 2.1
: SEQ ID NO 11
: LENGTH : 320
: TYPE: DNA
: ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/07959943
Patent No. 5418162
GENERAL INFORMATION:
APPLICANT: Blakely, Randy D.
APPLICANT: Fremeau Jr., Robert
APPLICANT: Caron, Marc G.
                                                            TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2278 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 2.1%;
Best Local Similarity 50.6%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-OOS
SOFTWARE: PATENTIN Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,943
FILING DATE: 19921014
CLASSIFICATION: 435
        MOLECULE TYPE: cDNA
POSTTION IN GENOME:
UNITS: 2278 basepairs
                                                                                                                                                                          NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405.38a
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
FEATURE:
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Sibley, Kenneth D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Serotonin Transporter cDNA NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 897 ctc999t9cctgac9gaagggaagctgcctgggactgcaaggtgaaggcaggt 948
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ADDRESSEE: Glbson
STREET: Post Office Drawer 31:
CITY: Raleigh
STATE: No. 5418162th Carolina
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2.1
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; LOCATION:
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Best Local Similarity 51.9
Matches 81; Conservative
                                                                                                 1943 GGGGAGGAGTCCAGTGGGGCTTTTCAGAGCTGAGAGGAGGTGGCTGGGAAGAGGTGTCCTC 1884
1823 TTCAGGAGTGATACTTTTAATAATGCGCTCCTTAAG 1788
                                               1883 TCCCAGGGTGTGTTACACAGCATTCATGCGGATGTCCCCCACACGGGATTTCTGTGGGTGT 1824
               731 ctctaggtccagatctatgagattgaacaacataag
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48..1868
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Search completed: October 3, 2002, 16:18:58 Job time: 16778 sec

AX281580 Sequence
AC073128 Homo sapi
AC009974 Homo sapi
AC027416 Homo sapi
U01206 Bos taurus
AL138688 Human DNA
AF461698 Gallus ga
S69088 gMHox-homeo
D1343 Gallus gall
D86982 Human mRNA
AC091776 Chlamydom

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Variants of the human amp-activated protein kinase gamma 3 subunit
Patent: WO 0177305-A 3 18-OCT-2001;
                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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AC073128
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DNA

linear

PAT 03-NOV-2001

AF305687

Homo sapi Sequence Homo sapi

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JOURNAL
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                           Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 98% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 187795 bases at least 040
Consensus quality: 190513 bases at least 030
Consensus quality: 192099 bases at least 030
Consensus quality: 192099 bases at least 020
Insert size: 200000; agarose-fp
Insert size: 194954; sum-of-contigs
Quality coverage: 5.58 in 020 bases; sum-of-contigs
Ouality coverage: 5.57 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qaggggagtcctcctggagcctggtgccctagaagcccacg
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                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (08-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Feb 21, 2001 this sequence version replaced gi:8469048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 2 clone 17 unordered pieces. ACC73128
                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: H_NH0647005
Summary Statistics
Sequencing vector: M13; 98%
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HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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be preserved.
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Nismatches 0;
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92241. .113337
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73917. .92140
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44743. .58275
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130426. .149287
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35356. .44642
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28988. .35255
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11957. .15783
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/db_xref="taxon:9606"
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Submitted (03-JAN-2002) Genome Sequencing Center, Washing University School of Medicine, 4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (08-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
5 (bases 1 to 206854)
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Submitted (08-SEP-1999) Genome
University School of Medicine,
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Unpublished (2001)
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4 (bases 1 to
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                        Center project name: H_NH0459I19
                                                                                    Contact: sapiens@watson.wustl.edu
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nilarity 100.
Conservative
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St. Louis, Missouri 63108,
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all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) VECTOR: pBACe3.6.

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.

Data from AC079810 and AC073128 was used to finish this clone,

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists beteen 38812-38903. Am unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

Location/Qualifiers

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FEATURES misc_feature source /note= /note= 281. . /note-220. .: 164. /note="similar to Homo sapiens EST BI114348 (NID:g14565249)" /note-"match /note="match /note="match /clone="RP11-459I19" /clone_lib="RPCI-11" note-"match /note-"match /note="match to /note="match /note="match /db_xref="taxon:9606" /chromosome="2" note="match to note="match to EST BI059713 (NID:g14467240)" /note="match to EST BE314060 (NID:g9134719)" ∕organism="Homo sapiens" . 206854 match match match 6 6 to ç 6 to EST ç ç ç to EST BF304755 (NID:g11251653)" EST BF183086 BE908408 A1670836 BG477625 (NID:g13409904)" BE047599 BG470047 C05773 (NID:g1502549)" BE908408 (NID:g10402954)" BE047599 (NID:g8364652) tz39c01.y1" AW880850 AL567345 (NID:g10402954)" (NID:g8364652) tz39c01.y1" (NID: g13402322)" (NID:g4850567) wa04g10.x1" (NID: 98042860)" (NID: 912920610) (NID:g11061273)"

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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Laroqque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McCwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McRenan, C., Minoya, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassilev, H., Vlel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campoplano, A., Castle, A., Cheepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Graham, C., Graham, G., Gra
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                              Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 135376 bases at least Q30 Consensus quality: 143264 bases at least Q30 Consensus quality: 146503 bases at least Q20 Consensus quality: 146503 bases quality: 146503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: 504_G_11
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60596 60695: gap of 100 bp 60696 66595: contig of 5900 bp in length 66596 66695; gap of 100 bp 66596 66695; gap of 100 bp in length 66696 73218: contig of 6523 bp in length 73219 73318: gap of 100 bp 73319 77115: contig of 3797 bp in length 77216 85022: contig of 7807 bp in length 85023 85122: gap of 100 bp 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is
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be preserved.
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55871: contig of 4486 bp in length
100 bp
10595: contig of 4624 bp in length
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51285: contig of 4820 bp in length
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38179: contig of 4111 bp in length
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98.4%; Score 99.4; DB 2; Length 152129; rity 99.0%; pred. No. 1.2e-16; nservative 0; Mismatches 1; Indels 0; Gaps	_fragment	/note="assembly_tragment" /note="assembly_tragment"	, ¦,	ragment	I ragment	_tra	111	, !	111	.51285	_irayment	, i	38179	/HOCKET ASSEMBLY_IRAGINERC /HOCKET ASSEMBLY_IRAGINERC /HOCKETT ASSEMBLY FRAGMENT /HOCKETT ASSEMBLY FRAGMENT	f :	, I	-h !	19567. 21928	<pre>clone_end:SP6 vector_side:left"</pre>	/note="assembly_fragment	note="	/note="assembly_fragment" 1514417123	-			, ,	/note= assembly fragment * /note= assembly fragment *		71	/note="assembly_fragment"	/note-massembly_fragment"	/clone="RP11-504G11" /clone_lib="RPCI-11 Human Male BAC"	/organism="Homo sapiens" /db_xref="Laxon:9606"	938 152129: contig of 14192 bp in length. Location/Qualifiers 1152129

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                                                                                      62 aggggagtcctcctggagcctggtgccctagaagcccac 100
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                                                             GGGGAAGCCCTCCAGGAGCCGGGGAAGGAGGCGGCCCAC 2084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l (bases 1 to 2539)
Premont, R.T., Koch, W.J., Inglese, J. and Lefkowitz, R.J.
Identification, purification and characterization of GRK5, a member of the family of G protein-coupled receptor kinases
J. Biol. Chem. 269, 6832-6841 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-SEP-1993) Richard T. Premont, Department of Medicine, Duke University Medical Center, Durham, NC 27710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U01206.1
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Bos taurus GRK5 protein kinase mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 2539)
                                                                                                                                                                                                                                                                                                                                                                                                                                         673
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="GRK5 protein kinase"
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/db_xref="GI 437106"
/db_xref="GI 437106"
/db_xref="GI 437106"
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MNTRRLEAGAKLDPPFYDPRAVYCKDYLDIEGFSTVKGVNLDHTDDDFYSKFSTGSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPWQSEMIETECFKELNVFGPHGTLSPDLNRSHPPEPPKKGLLQRLFKRQHQNNSKSSPNHKINSNHYSSNSTCSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="GRK5
175...1947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="tongue epithelium"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                   34.78;
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                                                                                                                                                                                                                                                                                                   Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein kinase"
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                           DB
. 15;
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                                                                                                                                                                                                                                                                                                                            4; Length 2539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete cds.
                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35960
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AUTHORS
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AL138688/c
                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
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                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL: Sw: SWISSPROT; Tr: TREMBL: Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Aug 29, 2000 this sequence version replaced gi:9863492.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human DNA sequence from clone RP11-264J4 on Chromosome 13. Contain ESTs, STSs, GSSs and CpG islands. Contains the 3' part of the ZNF198 gene for zinc finger protein 19 a novel gene, a gene for novel connexin (gap junction protein), a novel cyclophilin type peptidyl-prolyl cis-trans isomerase pseudogene and the GJB2 gene for gap junction protein beta 2, 26 kD (connexin 26), complete
                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPORTANT: This sequence is not the entire insert of clone RP11-264J4 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-264J4 is at 127794 in this sequence. The true left end of clone RP11-501K3 is at 100168 in this sequence. The true right end of clone RP11-110K18 is at 21477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl3 RP11-264J4 is from the library PGC-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21-NOV-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL138688.27 GI:9944124 HTG; connexin; CpG island; cyclophilin; gap junction protein; GJB2; prolyl cis-trans isomerase; zinc finger; ZNF198.
                                                                                                                                                                                                                                                                                                                                                                                                                              in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wall, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates;
1 (bases 1 to 127794)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             feature key.
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                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
/note=":941. .9"
                                                  /note="AluY repeat: matches 1. .294 435. .508
                                                                                                                             /note="AluJ/FLAM repeat: matches 1.
                                                                                                                                                                               /note="AluJ/FLAM repeat: matches 2. .69 of consensus"
                                                                                                                                                                                                                                 /clone="RP11-264J4"
/clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/chromosome="13"
                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                            1. .127794
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                            . 371
                      L1MB3 repeat: matches 6109. .6181 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127794 bp
                                                                           of consensus
                                                                                                                               .69 of consensus"
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Em: 113472 Em: AB002383 Em: AF161582 Em: X95808

match: EST's: Em: AW464846 Em: AA204514 Em: X95808

match: EST's: Em: AW464846 Em: AA204514 Em: X95808

Em: AA421981 Em: BE169588 Em: AL042736 Em: X9683458

Em: BE813524 Em: AA210440 Em: AW915439 Em: BE813463

Em: BE813524 Em: AA210440 Em: AW915439 Em: BE813463

Em: BE813524 Em: BE813473 Em: AA452383 Em: AW993938

Em: AW993981 Em: BE813473 Em: AA452383 Em: AW993938

Em: BE813474 Em: AW802227 Em: AW802290 Em: AB813501 Em: W36451

Em: BE813517 Em: AW993966 Em: AA161918 Em: AW893938

Em: AW8579387 Em: AA361348 Em: AA161918 Em: AW8579322 Em: A1112706

Em: AE813517 Em: AA861348 Em: AA161918 Em: AW879322 Em: A1112706

Em: AB813517 Em: AA861315 Em: AA452383 Em: AW99395153

Em: AW8579387 Em: AA361348 Em: AA161918 Em: AW9579322 Em: A1112706

Em: AA642651 Em: AA851515 Em: AW556500 Em: BE530161 Em: AW107660

Em: AA642651 Em: AA851515 Em: AM556500 Em: BE530161 Em: AW107660

Em: AW822686 Em: A1111670 Em: AA9600263 Em: AA370562 Em: C14750

Em: AB851395 Em: AH1811670 Em: AA9600263 Em: AA370562 Em: C14750

Em: BE631373 Em: AA1881925 Em: AV856500 Em: AB328077 Em: BE988433

Em: BE710363 Em: A71855 Em: A160699 Em: AB328077 Em: AB4683837

Em: BE710363 Em: AA135989 Em: AA115047 Em: BE937769 Em: AA663837

Em: BE781058 Em: AA283078 Em: AA115047 Em: BE937769 Em: AA663837

Em: AA66937 Em: AA283078 Em: AA115047 Em: BE937769 Em: AA663837

Em: AA66937 Em: AA452155 Em: AA1382776 Em: AA1472479

Em: AA66937 Em: AA452155 Em: AA138276 Em: EM11381192

Em: C14354 Em: AI367945 Em: AA034499 Em: AW188335 Em: AA251580

Em: BE936169 Em: AA362155 Em: AA370561 Em: C14328 Em: A1273953

Em: AA6629081 Em: C14749 Em: BE701998 Em: AA4746706 Em: AW79268

Em: BE701916 Em: AW882994 Em: AA903233

Em: BE700916 Em: AW882994 Em: AA903333

Em: BE700916 Em: AW882994 Em: AA903333

Em: BE700916 Em: AW882994 Em: AA903333

Em: BE700916 Em: AW88294 Em: AA251384

Em: BE700916 Em: AW88294

Em: BE700916 Em: AW8
               /note="continues in ball0K18 (AL137119) match: proteins: Tr:043308 Tr:Q9UBW7 Tr:043434 Tr:060898 Tr:Q9VB55 Sw:Q14202"
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join(<7550. .7664,8315. .8566,9190.
/gene="ZNF198"
                                                                                                                                                                         /evidence=not_experimental
7550. .12268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MER58 repeat: matches 5. .... Of consensus
6568. .6892
/note-"Limec repeat: matches 2140. .2148 of consensus
join(<7550. .7664,8315. .8566,9190. .9310,11356. .12268)
/gene-"ZNF198"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: cDNAs: Em:AF060181 Em:AJ224901 Em:AF012126
Em:Y13472 Em:AB002383 Em:AF161582 Em:X95808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6505. .6556
/note="MER38 repeat: matches 5. .57 of consensus
MER58 repeat: matches 5. .57 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: Em:AQ053217" 3374 .3652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Alusc repeat: matches 1..306 of consensus" 5887..6025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4202. .4434

MDR33 repeat: matches 44. .324 of consensus

MDR33 repeat: matches 44. .324 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2360. 2623
/note="AluSx repeat: matches 43. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1208. .1524
/note="AluSx repeat: matches 6. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="19 copies 2 mer tt 78% conserved"
1208. .1524
                                                                                                               .9310,11356.
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                                                                                                                  .11548)
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                               AF461698
                                                             RESULT
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                                                                                                                               GGGGGCATCCCGCAG 44384
     AF461698
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//note="match: GSS: Em:AQ142889"
16151. 16285
/note="MER46C repeat: matches 181. .333 of consensus
MER46C repeat: matches 181. .333 of consensus"
16354. 16432
/note="MER46C repeat: matches 2 .81 of consensus
MER46C repeat: matches 2 .81 of consensus
MER46C repeat: matches 2 .81 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="ZNF198"
12257. .12262
/gene="ZNF198"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="12 repeat: matches 2668.
17564..17668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L2 repeat: matches 2641.
complement(16918. .17359)
                                                                                                                                                                                                                                                                                                                                                                                                                                     18161. 18307
/note="MIR repeat: matches 6. .174 of consensus"
18633. .18949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"MER5A repeat: matches 57. .161 of consensus"
18161. .18307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="5 copies 14 mer 84% conserved"
12662. .12957
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17228. .17305
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12269. .12338
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12224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluSp repeat: matches 1. .308 of consensus"
9552. .9843
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VEEDYLWRIKGLGSHSPVALLWTLFYFNTKYFGLKTVEGHLKLSFGTVFRHWKKNPLT
MENKACLRYQVSSLCGTDNEDKITTGKRKHEDDEPVFEGIENTANPSRCPVKMFECYL
SKSPQNLNQRMDVFYLQPECSSSTDSPVWYTSTSLDRNTLENMLVRVLLVKDIYDKDN
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     692
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.16180)
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linear
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VRT 24-JAN-2002

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Matches 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chicken heart stage 17 embryo.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 895)
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47; Conserv
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AF461698
             GenBank staff at the National Library of Medicine created this entry [NCBI glbbsq 144347] from the original journal article.
                                                                              The expression pattern of the chick homeobox role in patterning of the limbs and face and compartmentalization of somites
                                                                                                                                                                                                                                                                        gMHox=homeobox [chickens, 
$69088
$69088.1 GI:545359
                                                                                                                                                                                                                                                                                                                      880698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (21-DEC-2001) Otolaryngology, University of Florida, 12901 Bruce B. Downs Blvd., Tampa, FL 33612,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venkataramu, C.R. and Sokolowski, B.H.A. Protein protein interactions of Kvbeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archosauria; Aves; Neognathae; Phasianinae; Gallus
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                                                 94148118
                                                                                                                              Olson, E.N.
                                                                                                                                           Kuratani, S., Martin, J.F., Wawersik, S., Lilly, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                               Biol. 161 (2), 357-369 (1994)
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/product="paired-related homeobox"
/protein_id="Aal67846.1"
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NASLLKSYSGDVTAVEQPIVPRPAPRPTDYLSWGTASPYSAMATYSTTCTNASP"
a 220 c 217 g 97 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Gallus gallus"
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/dev_stage="embryonic"
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67.1%;
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Pred. No. 59;
0; Mismatches
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                                                                                                             gMHox suggests
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Gallus gallus p
D13433
D13433.1 GI:23
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Gallus gallus (library:
clones p2 and p7.
Gallus gallus
                                                                                                                                                                                                                                                                   Submitted (20-OCT-1992) Tsutomu Nohno, Kawasaki Medical School Dept. of Molecular Biology; 577 Matsushima, Kurashiki, Okayama 701-01, Japan (Tel:0864-62-1111(ex.3637), Fax:0864-62-1199) 2 (bases 1 to 1084)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
47; Conserv
                                                                                                                                                                                     A chicken homeobox gene related to Drosophila paired predominantly expressed in the developing limb Dev. Biol. 158 (1), 254-264 (1993)
                                                                                                                                                          Submitted (20-OCT-1992) to DDBJ by:
                                                                                                                                                                                                                                      and Noji, S.
                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                              Kurashiki 701-01
                                                                                              577 Matsushima
                                                                                                                          Department of Pharmacology
                                                                                                                                           Tsutomu Nohno
                                                                                                                                                                            93321789
                                                                                                                                                                                                                                                                                                                                                  Nohno, T
                                                                                                                                                                                                                                                                                                                                                                                  Phasianinae; Gallus.
                                            Phone:
                                                                                                           Kawasaki Medical School
                                                                                                                                                                                                                                                    Nohno, T., Koyama, E., Myokai, F., Taniguchi, S.,
                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 1084)
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/db_xref="GI:545360"
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/note="homeobox"
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1. .895
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                                                                                                                                                                                Submitted (02-AUG-1996) Osamu Ohara, Kazusa DNA Research 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.cr.jp, Tel:+81-438-52-3913)
                                                                                                                                                                                                                                                                                                                        Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y., Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N. Prediction of the coding sequences of unidentified human genes. V The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced analysis of cDNA clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)
                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                        2 (bases 1 to 6335)
Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/product-"paired-related homeotic gene product"
/protein_id-"BaA02695.1"
/protein_id-"BAA02695.1"
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/translation-"MASSYAHAMERQALLPARLDGPAGLDNLQAKKNESVSHLLDLEE
/translation-"MASSYAHAMERQALLPARLDGPAGLDNLQAKKNESVSHLLDLEE
/translation-"MASSYAHAMERQALLPARLDGPAGLDNLQAKKNESVSHLLDLEE
/translation-"MASSYAHAMERQALLPARLDGPAGLDNLQAKKNESVSHLLBSPGLTSGSDTPQQDNDQLNGSEKKKEKORRNRTTFN
SGDVALGREFERTHYDAFVREDARRVNLTEARVQVWFQNRAKFTRNERMLASKN
ASILKSYSGDVTAVEQPIVPRAARRPTDYLSWGTASPYSAMATYSTTCTNASPAQGMN
ANNSLANLRLKAKEYSLQRNQVPTVN"
/cell_line="KG-1"
/cell_type="myeloblast"
/tissue_type="bone marrow"
                                                                           /organism⇒"Homo sapiens"
/db_xref⇒"taxon:9606"
/chromosome⊸"chromosome 6.
/clone⇒"HA2570"
                                                           /sex="male"
                                                                                                                                                                      Location/Qualifiers
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233. .967
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/db_xref="taxon:9031"
/clone_lib="lambda gt10"
/dev_stage="Stage 24-26"
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67.1%;
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Pred. No. 53;
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                              OK 73019, USA on Jan 29, 2002 this sequence version replaced gi:16271941
------------- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
                                                           Submitted (02-JUN-2001) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                  Jia, H., Lin, S., Wu, H., Direct Submission
                                                                                                                                    1 (bases 1 to 54018)
Jia, H., Lin, S., Wu, H., Dutcher, S. and Roe, B.A.
Chlamydomonas reinhardtii BAC Clone cr-4121
                                                                                                                                                                                                 Chlamydomonas reinhardtii. Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                          Chlamydomonas reinhardtii clone cr-4i21, WORKING DRAFT SEQUENCE, 5
                                                                                                                        Unpublished
                                                                                                                                                                         Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                          Chlamydomonadaceae;
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                    unordered pieces.
AC091776
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                                                                                               Dutcher, S. and
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                                                         Parrington Oval,
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                                                                                                 Roe, B.A.
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AC090435/c
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                                                                                                                                                   OK 73019,
On Jan 29,
                                                                                            Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
                                                                                                                                                                            Wu,H., Lin,S., Jia,H., Dutcher,S. and Roe,B.A.
Direct Submission
Submitted (21-FEB-2001) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                           1 (bases 1 to 65898)
Wu.H., Lin,S., Jia,H., Dutcher,S. and Roe,B.A.
Chlamydomonas reinhardtii BAC Clone cr-32m22
                                                                                                                                                                                                                                                                                                                                                                                    Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
                                                                               Center code: UOKNOR
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Chlamydomonas reinhardtii clone
                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                              Chlamydomonadaceae; Chlamydomonas.
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   NOTE: This is a 'working draft' consists of 4 contigs. The true is not known and their order in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/db_xref~"taxon:3055"
/clone="cr-4i21"
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18192 c 16851 g
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1. .54018
                                                                                                                                          2002 this sequence version replaced g1:18139395.
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5117: gap of unknown length
10018: contig of 4901 bp in length
10118: gap of unknown length
21786: contig of 11668 bp in length
21886: gap of unknown length
33146: contig of 11260 bp in length
33246: gap of unknown length
54018: contig of 20772 bp in length.
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Pred. No. 32;
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AL133352
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 ggggagtcctcctggagcc 81
                                         AL Submitted (04-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 26, 2000 this sequence version replaced gi:7327699.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may phage etc. Order of segments is not known: 800 n's separate segments. Contig_ID: 00484 Length: 157824bp
Contig_ID: 01411 Length: 15050p.
**NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pleces is not known and their order in this sequence record is runs of N, but the exact sizes of the gaps are unknown.
**This record will be updated with the finished sequence will separate of the page are unknown.
**This record will be updated with the finished sequence will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTGGCCCGGCCCTGGGCC 30180
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161999 bp DNA linear HTG 04-A
HOMO Saplens chromosome 10 clone RP11-411B6, *** SEQUENCING
PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pearce,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/clone_lib="cr-32m22"
22600 c 21674 g 10642 t
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/db_xref~"taxon:3055"
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4554: gap of unknown length
18724: contig of 14170 bp in length
18824: gap of unknown length
30657: contig of 11833 bp in length
30757: gap of unknown length
65898: contig of 35141 bp in length.
157824: contig of 157824 bp in length
8624: gap of 800 bp
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Pred. No. 30;
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Best Local
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                  Benton, J., Binage, K., Blankenburg, K., Banks, T., Barbaria, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hoguses, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Martinez, E., Mawhiney, E., Mattinez, E., Massey, E., Mawhiney, E., Miner, Z., Mitchell, T., Mohabbat, K., Mary, J., Newtson, N., Nohabbat, K., Mayuen, N., Nayuen, N., Nayuen, N., Nickerson, E., Nokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nokenkwo, S., Oulles, M., Rolye, N., Pace, A., Payton, B., Peters, L., Pickens, R., Prinus, E., Pul, L., Oulles, M., Rolye, M., Rolye, N., Stanley, H., Shooshtari, N., Stanley, H., Shoosh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
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160140 160939: gap of 800 bp
160940 161999: contig of 1060 bp in length
Location/Qualifiers
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/clone_lib="RPCI-11.2"
35796 c 36927 g 43
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/db_xref="taxon:9606"
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            Sodergren, E., Sonaike, T.,
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Pred. No. 25;
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Scott,G., Shen,H., Shoosntae,T., Sparks,A., Stanley,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_d.NOTE: This is a 'working draft' sequence. It currently consists of 69 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will be preserved.
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STS Content:
SHGC-35371 G28590
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                                                                                                                                                                                                                                                www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 203200)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                               www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.5% of Sequence:
Estimated Total Number of Errors is 0.8.
                                                                                                                                                                                                                                                                                   Drive, Walnut Creek, CA 94598, USA
On Jan 22, 2001 this sequence version replaced gi:11178043
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203200 bp DNA linear PRI 22-JAN-2001
Homo sapiens chromosome 19 clone CTD-2561020, complete sequence.
AC008744
AC008744.6 GI:12331466
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Copyright (c) 1993 - 2000 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	101	Score
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AAS81565	AAK76637	AAT 41154	AAI17045	AAK35441	AAK09549	ABA29092	ABA61253	AAH43683	ID
DNA encoding novel	Human immune/haema	Probe #9840 used t	Probe #6978 for ge	Human bone marrow	Human brain expres	Probe #7558 for ge	Human foetal liver	PRKAG3 intron 4 -	Description

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reproducti strain SB5 strain SB5 strain SB5 strain SB5		#17409 for brain expre- bone marrow #16156 for #22880 used immune/haem cDNA clone cancer asso ATFx coding CDNA sequen immune/haem colon cance	DNA encoding novel Human bone marrow Human bone marrow Human bone marrow Human foetal liver

ALIGNMENTS

RESULT

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                                                                              exon
                                   exon
                                                                                                          Key
intron
                                                                                                                                           Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ds.
             intron
                                                                                                                                                                  PRKAG3 intron 4 - intron 10
                                                                                                                                                                                 21-JAN-2002 (first entry)
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                                                                                                                        Sequence 1722 BP;
                                                                                                                                                                                                                                                                            Example 1; Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370..1522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1042..1242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                           25pp;
                                                                                                                        321 A; 504 C;
                                                                               100.0%;
                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Exon
                                                                                                                                                                                                                                                                                                                                                                       Marklund
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              portion of intron
                                                                       0;
                                                                              Score 101; DB 22;
Pred. No. 1.3e-18;
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                                                                                                                        534
                                                                      Mismatches
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                                                                                                                        G;
                                                                                                                        363
                                                                                                                        T; 0
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                                                                                                                        other;
                                                                      Indels
                                                                                        Length 1722;
                                                                    0;
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ABA29092
ID ABA:
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                                           RESULT
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                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                      Matches
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-068408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                   measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
ABA29092
                                                                                                                                                                                                                            Sequence 550
                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 9558; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn
                    ABA29092 standard;
                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; foetal liver; gene expression; single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human foetal liver single exon nucleic acid probe #9558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA61253;
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                                                                             245
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                                                                                       cctcctggagcctggtgccctagaagc
                                                                                                                                  ccaaaagtaaccagcttccctccaaac
                                                                                                                       ctgatgaagactaggcgggggcaaggctgtggcaccagatgggcagggggtgctggggagg
                                                                                                                                                                                                                                                                                                                                                                                                                                               SG,
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                                                                                                                                                                      1 Similarity
53; Conserv
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                                                                                                                                                                      Conservative
                                                                                                                                                                                                                            BP; 154 A; 139 C; 127
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                    DNA;
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                                                                                                                                                                             32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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                    550
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                    ВР
                                                                                                                                                                   Score 32.6; DI Pred. No. 4.3; O; Mismatches
                                                                                                                                                                      0,
                                                                                                                                                                              32.6; DB
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                                                                                                                                                                                                                            130 T; 0 other;
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                                                                                                                                                                     34;
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                                                                                                                                                                     Indels
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RESULT
AAK09549
ID AAKO
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AC AAKO
XX
DT 05-N
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                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for prodicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systems.
          05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                AAK09549;
                                                   AAK09549 standard;
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not specification, but was obtained in electronic fo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 7558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                       congenital heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
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26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human: gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                          hearts
                                                                                                          245
                                                                                                                                                    185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00666
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                                                                                                                               70
                                                                                                                                                                         10
                                                                                                        ccaaaagtaaccagcttccctccaaac 271
                                                                                                                    cctcctggagcctggtgccctagaagc
                                                                                                                                              ctgatgaagactaggggggggaaggctgtggcaccagatgggcaggggtgctggggagg
                                                                                                                                                          SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon nucleic acid
                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                    550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
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2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0234687
2000US-02346359
2000US-0236359
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
         (first entry)
                                                                                                                                                                                                                                                  BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression
                                                                                                                                                                                                                                                  154 A;
                                                    DNA;
                                                                                                                                                                                                       32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen
                                                                                                                                                                                                                                                  139
                                                    550
                                                                                                                                                                                                                                                                                                                                                                                                                530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               probes for analyzing
                                                                                                                                                                                           Score 32.6; D
Pred. No. 4.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Σ
                                                    ВÞ
                                                                                                                                                                                                                                                 C; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank
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                                                                                                                            96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR,
                                                                                                                                                                                                                                                130 T; 0
                                                                                                                                                                                                  DB
4.3;
                                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression in
                                                                                                                                                                                                                                                                                 format
                                                                                                                                                                                                                                                other;
                                                                                                                                                                                                                                                                                          form
                                                                                                                                                                                                              Length
                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                               part of the printed directly from WIPO
                                                                                                                                                                                                               550;
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                                                                                                                                                                                         Gaps
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PXX XXX DXXX AC XXX DXXX XXX
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AAK35441
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Best Local
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                 Homo sapiens
                                                                  Human bone marrow
                                                Human;
                                                                                     06-NOV-2001
                                                                                                                          AAK35441 standard; DNA; 550
                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                           Single
brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
                                                                                                                                                                                                                                                                                                        Sequence 550
                                                                                                                                                                                                                                                                                                                                                                                                        Example 4;
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27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microarray; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human brain expressed single
                                                                                                                                                                           245
                                                                                                                                                                                                                  185
                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                     10
                                                                                                                                              G
                                                                                                                                                                                    cctcctggagcctggtgccctagaagc
                                                                                                                                                                                                            ctgatgaagactaggcgggggcaaggctgtggcaccagatgggcaggggtgctggggagg 244
                                                                                                                                                                                                                         ccaaaagtaaccagcttccctccaaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG,
                                             bone
                                                                                                                                                                                                                                                         53; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:
                                marrow expressed exon; gene expression analysis; probe; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                        Conservative
                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                        BP;
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                                                                                                                                                                                                                                                                                                       154 A;
                                                                expressed single
                                                                                                                                                                                                                                                                32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                    9540; 650pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon;
                                                                                                                                                                                                                                                                                                       139 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon; gene expression analysis; probe; disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                     probes
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                                                                                                                           ВP
                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                Score 32.6; D
Pred. No. 4.3;
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                                                                                                                                                                                                                                                                                                        127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 for analyzing gene expression
                                                                                                                                                                          271
                                                                                                                                                                                            96
                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe
                                                                                                                                                                                                                                                                                                       G;
                                                                                                                                                                                                                                                                                                       130
                                                                probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                                                          DB
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WO200157276-A2

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Best Local S
Matches 53
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
                                                                                                                                      cervical cancer;
                                                                                                                                             Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                              probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                          30-JAN-2001;
                                                                             09-AUG-2001
                                                                                                WO200157278-A2
                                                                                                                                                                  Probe
                                                                                                                                                                                      12-OCT-2001
                                                                                                                                                                                                        AAI17045;
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analyzing
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27-SEP-2000;
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                              ctgatgaagactaggcgggggcaaggctgtggcaccagatgggcaggggtgctggggagg
                                                                                                                                                                                                                                                                          ccaaaagtaaccagcttccctccaaac
                                                                                                                                                                                                                                                                                    2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SC,
                                                                                                                                                              #6978 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome-derived single exon nucleic acid probes useful zing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                    1 Similarity 60.9
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                     550
                                                                                                                                                                                                                            standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO:
2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-063234687.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                     BP;
                                                          2001WO-US00670
                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                     154 A; 139 C; 127
                                                                                                                                                                                                                                                                                                                                                                                                                       invention.
                                                                                                                                                                                                                            DNA:
                                                                                                                                                                                                                                                                                                                                                             32.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9998; 658pp + Sequence Listing;
                                                                                                                                                                                                                            550
                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                    Score 32.6; Di
Pred. No. 4.3;
O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank
                                                                                                                                                                                                                                                                           271
                                                                                                                                                                                                                                                                                            96
                                                                                                                                                                                                                                                                                                                                                                                                    G; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR;
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RESULT
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                                                            04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                     genetic disorder;
                    (MOLE-)
                                                                                                                              30-JAN-2001;
                                                                                                                                                    09-AUG-2001
                                                                                                                                                                           WO200157272-A2
                                                                                                                                                                                                                             Probe; microarray; human;
                                                                                                                                                                                                                                                 Probe #9840 used to measure gene expression in human placenta
                                                                                                                                                                                                                                                                         17-OCT-2001
                                                                                                                                                                                                                                                                                                                   AAI41154 standard; DNA; 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful fanalyzing gene expression in human cervical epithelial cells
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04-OCT-2000;
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53; Conserv
                   MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID No 6978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to human single exon nucleic acid probes present sequence is one such probe. The SENPs are derived HeLA cells. The SENPs can be used to produce a single exon thick
                                       2000US-0180312.
2000US-0207456.
2000US-0609408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0234263.
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                                                                                                                              2001WO-US00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 154 A; 139 C;
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2000GB-0024263.
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                                                                                                                                                                                                                             placenta;
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Pred. No. 4.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                   ВP
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SG,

Hanzel DK,

Chen W,

Rank DR;

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Best Local S
Matches 53
     31 - JAN - 2000;
04 - FEB - 2000;
04 - FEB - 2000;
02 - WAR - 2000;
16 - WAR - 2000;
17 - WAR - 2000;
17 - WAR - 2000;
19 - WAY - 2000;
07 - JUN - 2000;
07 - JUN - 2000;
07 - JUL - 2000;
07 - JUL - 2000;
11 - JUL - 2000;
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analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                 WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic;
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                                                                                                                                                                                                                                                                                                              17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune; haematopoietic; immune/haematopoietic antigen; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245
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zing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune/haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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     2000US-0179065
2000US-0184664
2000US-018466350
2000US-0189874
2000US-0199123
2000US-0199123
2000US-0199123
2000US-0209467
2000US-0216486
2000US-0216647
2000US-0216647
2000US-0217496
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                                                                                                                                                                                                                                                                                                                                                                                                                  therapy; vaccine; metastasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigen
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Pred. No. 4.3;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic sequence
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    14 AUG 2000
18 AUG 2000
22 AUG 2000
22 AUG 2000
23 AUG 2000
23 AUG 2000
01 SEP 2000
01 SEP 2000
01 SEP 2000
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06 SEP 2000
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2000US-0226868
2000US-0227099
2000US-0229709
2000US-0229343
2000US-0229343
2000US-0229513
2000US-0231413
2000US-0231414
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2000US-0231406
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2000US-0231400
2000US-0231600
2000US-0231600
2000US-0231600
2000US-0231703
2000US-0231800
2000US-0241786
2000US-0241786
2000US-0241809
2000US-02446176
2000US-02446176
2000US-0246476
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2000US-02464776
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2000US-02466478
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2000US-0225267.
2000US-0225268.
2000US-0225270.
2000US-0225447.
2000US-0225757.
2000US-0225757.
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activity, and can be used in gene therapy and vaccine production. (I)

C proteins and polynucleotides may be used in the prevention, diagnosis and

C treatment of diseases associated with inappropriate (I) expression. For

C example, they may be used to treat disorders associated with decreased

C expression by rectifying mutations or deletions in a patient's genome

C that affect the activity of (I) by expressing inactive proteins or to

C supplement the patients own production of (I). Additionally, (I)

C polynucleotides may be used to produce the secreted (I), by inserting

C the nucleic acids into a host cell and culturing the cell to express the

C diagnose and treat immune/haematopoietic-related diseases, especially

C cancers and cancer metastases of haematopoietic-derived cells. AAK64703

C sequences from the present invention. AAK54942 to AAK54950 and AAM82169

C represent sequences used in the exemplification of the present invention.
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                          AAK54951 to AAK64702 encode the human immune/haematopoietic antigen
                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding useful for preventing,
                                                                                                                                                                                                                                amino acid sequences given in AAM82170 to AAM91921.
                                                                                                                                                                                                                                                                           Disclosure;
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                                                                                                                                                                                                                                                                                                                                                          2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN GENOME
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2000US-0251479.
2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251989.
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2000US-0249209
2000US-0249211
2000US-0249211
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2000US-0249213
2000US-0249213
2000US-0249214
2000US-0249215
2000US-0249217
2000US-0249218
2000US-0249218
2000US-0249248
2000US-0249248
2000US-0249249
2000US-0249264
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2000US-0249264
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2000US-0249265
2000US-0249266
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2000US-0254097.
2001US-0259678.
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2000US-0246610.
2000US-0246611.
2000US-0246613.
2000US-0249207.
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                                                                                                                                                                                                                                                                                                             human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
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                                                                                                                                                                                                                             (I) have cytostatic
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Sequence 680 BP; 116 A; 213 C; 185 G; 166 T; 0 other;

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Best Local
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(II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                   biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder;
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2000US-0649167.
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58.9%;
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Pred. No. 4.3;
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Best Local
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polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                  diagnostics,
                                                                                                                                                                                                                                                                                         biodiversity
                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
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23-AUG-2000;
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2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder;
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RESULT 11
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19-JUL-2000;
03-AUG-2000;
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19-OCT-2000;
30-NOV-2000;
       The present sequence is one of 251 novel human polynucleotides expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders.
                                                               Claim
                                                                                                                                               Zhao
                                                                                                                                                                                                                                                                                                                                                                                              Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer
                                                                              diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                        (HYSE-)
                                                                                                                                                                                                                                                                        21-JAN-2000;
25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
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                                                                                                                                                                                                                                                                                                                                                                                       immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone marrow cDNA, SEQ ID NO:
                                                                                                                 AAM00988
                                                                                                                                                                                         HYSEQ INC.
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                                                               Page 574-579;
                                                                                                                                                        Boyle BJ,
Nang J, Wej
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                               Zhou P,
                                                                                                                                                                                                                     2000US-0653450.
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  caused
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                                                                                                                                                       Tang YT, L:
chman T, Xu (
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ie AJ, Yang
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25-APR-2000;
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14-SEP-2000;
19-OCT-2000;
30-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of chemical compounds as potential drugs.
                                                         Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders -
                                                                                                                                                                                                                                                                                                (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-2000;
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F, Wang J, Werhman
QA, Zhou P, Drmana
                                                                                                                                      2001-488707/53.
DB: AAM00937.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cctcctggagcctggtgccctagaagccca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bone marrow cDNA, SEQ ID NO: 300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
54; Conserv
                                                                                                                                                                                                                                                                                                HYSEQ INC
                     Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3889 BP; 861 A; 1090 C; 1008 G;
                                                                                                                                                                                                                                                                                                                                                                                  2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US34960
                                                                                                                                                                                                                                                                                                                                            2000US-0693036
2000US-0250583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                       Drmanac RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA;
                                                                                                                                                                                                                   Tang .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus; HIV;
                                                                                                                                                                                                               YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32.4; D
Pred. No. 5.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                           u C,
                                                                                                                                                                                                                           C, Asundi V,
Xue AJ, Yan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   930 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DΒ
                                                                                                                                                                                                                      Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection; cancer;
sorder; haemophilia;
                                                                                                                                                                                                                                              Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                   Zhang
                                                                                                                                                                                                                                              ₽,
                                                                                                                                                                                                                      ŗ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             presence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS
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RESULT 13
AAH89943/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                         09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
         WPI; 2001-488707/53
P-PSDB; AAM00824.
                                              Zhao
                                                                      Ford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of chemical compounds as potential drives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous
                                                                                                                                                                                              21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                   WO200153453-A2
                                                                                               (HYSE-)
                                                                                                                      30-NOV-2000;
                                                                                                                                  14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                   23-DEC-2000; 2000WO-US34960
                                                                                                                                                                                                                                                           26-JUL-2001
                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                            immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; c
                                                                                                                                                                                                                                                                                                                                                                                                           Human bone marrow cDNA, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                      antiviral; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH89943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH89943 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3892 BP; 860 A; 1091 C; 1009 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of 251 novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              633 CTGATGAAGACTAGGCGGGGCAAGGCTGTGGCACCAGATGGGCAGGGGTGCTGGGGAGG 574
                                od JE, bu, ne n F, Wang J, we no OA, Zhou P,
                                    o QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 cctcctggagcctggtgccctagaagccca 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAAAAGTAACCAGCTTCCCTCCAAAAGCA 544
                                                                                                                                                                                                                                                                                                                                  immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                   bone
                                                                                            HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                     Boyle BJ,
                                                                                                                    2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-062312.
2000US-062312.
2000US-0653450.
2000US-0663191.
2000US-0693036.
2000US-0593036.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                          Werhman
                                              Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA; 4886
                                                     Tang YT, L.
                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; cytostatic; neuroprotective;
erial; antifungal; anti-HIV; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.1%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                         u C, x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                 autoimmune disorder; haemophilia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.4;
No. 5
                                                                                                                                                                                                                                                                                                                                                                                                            74
                                                         Xue
                                                                   Asundi V,
                                                         Ę,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                         Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotides
                                                         Chen
Y, z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                         Zhang
                                                                                                                                                                                                                                                                                                                                            cancer;
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ABA73753

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Best 1
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                                                                                                                                                                                                                                                                       30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                 Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosts and/or prognosts of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of chemical compounds as potential drugs.
                                                                                                                                                                                                                                             04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is one of 251 novel human polynucleotides expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders be genetic, may be caused by a viral (e.g. HIV), bacterial or fung
                                                                                                                                                                                               (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA73753;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA73753 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGATGAAGACTAGGCGGGGGAAGGCTGTGGCACCAGATGGGCAGGGGTGCTGGGGAGG 1557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bone-marrow-expressed polynucleotides and polypeptides, useful reating e.g. cancer and immune deficiency disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toetal liver single exon nucleic acid probe #22058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             foetal
                                                                                                                                                                                             MOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 259-260;
                                                                                                                                            Hanzel
                                                                                                                                                                                                                                        2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          liver;
                                                                                                                                            DK,
                                                                                                                                                                                          DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1117 A; 1370 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231
                                                                                                                                            ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32.4;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G; 1133 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacterial or fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
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Matches 52
                                                                                                                                                                   04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                               Claim
                                                                                                                    Penn
                                                                                                                                                                                                                                                              09-AUG-2001.
                                                                                                                                                                                                                                                                                                                       Human; gene expression; h cardiovascular disease; h congenital heart disease;
                                                                                                                                                                                                                                          30-JAN-2001;
                                                                                                                                                                                                                                                                                WO200157274-A2
                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                              Probe #17409
                                                                                                                                                                                                                                                                                                                                                                                 23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                    ABA38943;
                                                                                                                                                                                                                                                                                                                                                                                                                        ABA38943 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4;
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mes 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccaaaagtaaccagcttccctccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cctcctggagcctggtgccctagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctgatgaagactaggcgggggcaaggctgtggcaccagatgggcaggggtgctggggagg
                                               4 ;
                                                                            exon
                                                                                                                                        MOLECULAR DYNAMICS INC
                                               SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 22058; 639pp + sequence listing;
                                                                                                                    Hanzel
                                                                            nucleic
                                                                                                                                                         2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                             for gene
                                                                                                                                                                                                                                          2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relates to a single exon nucleic acid
                                               No 17409;
                                                                                                                   DK,
                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                            acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.9%;
                                                                                                                    Chen
                                                                                                                                                                                                                                                                                                                                                            expression analysis in human heart cell sample
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                                                                                                                                                                                                                                                                                                                               heart; microarray; vascular system; probe; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                        231
                                                                            probes
                                              530pp;
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Pred. No. 5.3;
O; Mismatches
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                                                                            for analyzing
                                               English.
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c format directly
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derive

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Search completed: October Job time: 14288 sec
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                                                                                                                                                                                                                                                                                                                                                                                from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at (tp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                             Sequence 231 BP; 54 A; 57 C; 63 G; 57 T; 0 other;
                                                                                                                                                               146 cigatgaagactaggcgggggcaaggctgtggcaccagatgggcagggggtgctggggagg 205
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B1960023 HVSMEN002
BE559614 601347308
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AW02638B wv12f05.x
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AL585199 AL585199
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BE600139 P11_91_G1
BE600139 P11_91_G0
BE598197 P11_66_H0
BE600794 P11_90_C0
BE595429 P11_55_D0
AG083214 PAN LTO91
B1951430 HVSME1002
                                                                                                                                                                                                                                                                        Description
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SOURCE
ORGANISM
                                                                                                                     FEATURES
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VERSION
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RS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
RS Wing,R., Close,T.J., Xleinhofs,A., Wise,R., Chin,A., Begum,D.,
RS Wing,R., Close,T.J., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons
.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex rachis cDNA library
Contact: Wing RA
Clemson University Genomics Institute
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 654 6293
Fax: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 121
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 2
High quality sequence stop: 553.
Location/Qualifiers
11 682
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B1960023
B1960023.1 G1:16311278
EST.
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Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
; Triticeae; Hordeum.
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682 bp mRNA linear EST 22-OCT-2001
HVSMED00222008f Hordeum vulgare rachis EST library HVcDNA0015
(normal) Hordeum vulgare cDNA clone HVSMED0022008f, mRNA sequence.
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/clone="HYSMEn0022008f"
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(normal)"
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yta; Liliopsida; Poales; Poaceae; Pooidea
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AL514251 AL514251
AZ527770 ENTDA88TF
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B1767103 603054158
BE783728 601471127
AL538973 AU533873
AW963549 EST375522
BE300397 600944511
B1254382 602976691
BE271259 600944511
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DEFINITION
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                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                           Plate: LLCM380 row: p column: 01 High quality sequence stop: 687.
                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 833)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE559614 833 bp
601347308F1 NIH_MGC_8 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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ilarity 60.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)*

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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
Xho1; Plants were grown at Washington State University,
Pullman, WA in a greenhouse, the rachises were excised and
frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close
lab at the University of California, Riverside total RNA
/clone="IMAGE:3688176"
/clone_lib="NIH_MGC_8"
                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                    Location/Qualifiers
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Pred. No. 47;
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                                                                                                                                                                                                                       BACKWARD: GTTTTCCCAGTCACGACG
Plate: 142 row: D column: 8
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                              and -minmatch 12 options.
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -min:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 377)
Smith, T.P. L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Smith, T.P. L., Grosse, White, J., Cho, J., Fahrenkrug, S.C., Bennett Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                          FORWARD: AGGAAACAGCTATGACCAT
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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12477 MARC 2BOV Bos taurus cDNA 5',
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/note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-*Organ: lymph; Vector: pOTB7; Site_1: xho1; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xho1 sites using the following 5' adaptor: GCCACCAAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).*
                                                                  /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
                                                                                                                                                                                                       Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
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Pred. No. 74;
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    ACGKGGKGGACKGKG
                                                                GGGGAGGAGKGGAAKKKKGCKGCKGCCCAAGAGKGGCKGGGGKGCAKGGGCKCCA 437
                                                                             aggggagtcctcctggagcctggtgccctagaagcccac 100
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AL530561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91006 EVRY cedex - France
                                                                                                                                                                                                                       Q)
                                                                                                                                                                                                                   vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com" 189 c 337 g 38 t 113 others
                                                                                                                                                                                                                                                                                                                            /note-"Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="CS0DD007Y022"
                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                            /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="LTI_NFL001_NBC4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 447
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Clemson University Genomics
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Conservative
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                                                                                                                                                                                                                                                                                                                                                   http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Alsc see Close TJ. Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)*

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Insert Length: 874 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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RESULT 8
BF808916/c
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AW026388/c
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                                                                                           BF808916 539 bp
PM4-CI0154-151100-001-h12 CI0154
 Eukaryota;
                  Homo sapiens
                                    numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -400P from Gibco
High quality sequence stop: 338.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW026388 354 bp mRNA linear EST 09-MAR-2000 wv12f05.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529345 3'similar to contains element MSR1 repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: David N. Louis, M.D., Myrna R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                           Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:2529345"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ∕organism="Homo sapiens"
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                      0;
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Pred. No. 2.7e+02;
0; Mismatches 15;
                                                                                           Homo sapiens cDNA,
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                                                                                                                                                                   Gallus gallus
                                                                                                                                                                                                                                                                                AL585199 685 bp mRNA linear EST 28-1
AL588199 BP Chicken Embryo Library Gallus gallus cDNA clone
ROS020D01, mRNA sequence.
AL585199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Coldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                   Archosauria; Aves; Neognathae; Phasianinae; Gallus
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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Seq primer: puc 18 forward
                                                                                                                                                                                                   chicken.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 an
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     Chicken Embryo Library
                                                               (bases 1 to 685
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c: +55-11-2707001
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/db_xref="taxon:9606"
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                                                                                                                                                        100 Jordan Hall, |
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                             Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library Unpublished (2001)
On Feb 22, 2001 this sequence version replaced gi:13109940.
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46; Conserv
                                                                                                                                                                                                                                        Clemson University
                                                                                                                                                                                                                                                                  Clemson University Genomics Institute
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HVSWEC0002B16f Hordeum vulgare seedling shoot EST library
HVCDNA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone
                                                                                                    Total hq bases = 300
                                                                                                                              Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                  Contact: Wing RA
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Roslin, Midlothian, EH25
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
Contact: Frazer Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVSMEc0002B16f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 735)
                 Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              frazer.murray@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Embryo"
/dev_stage="5 days old"
/lab_host="0H10B"
/note="Vector: pBLUESCRIPT SK; Site_1: Not1; Site_2: Sall;
/note="Vector: pBLUEScript Sk; Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Gallus gallus"
/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="ROS020D01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                              Clemson,
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
3.6e+02;
nes 24;
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EST 22-OCT-2001

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ORGANISM
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LOCUS
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    559 CTGGTGGGCAGGGGGGGGGGGGGGGGGAGCCCACCGGGGCGTGAGCGGAAGGGAGT 618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cctcctggagcctggtgccc 89
Department of Botany
The University of Georgia
Plant Sciences Building, Rm.
                                                                                     Contact: Cordonnier-Pratt MM
                                                                                                                    Unpublished (2000)
                                                                                                                                     An EST database from Sorghum:
                                                                                                                                                                                        Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.

1 (bases 1 to 382)
                                                                                                                                                                                                                                                                                                                                sorghum.
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                  BE600720.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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_91_G10.b1_A002 Pathogen induced 1 (PII) Sorghum bicolor cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              crystallization dishes. Five day old seedling shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pbluescript SK(-) cDNA phagemids. These steps were performed in the TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
156 c     264 g     116 t     10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Vector: lambdaZAP; Site_1: EcoR1; Site_2: xhol; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="TJC121"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Hordeum vulgare"
/cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                  GI:9855905
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Pred. No. 4e+02;
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  2502, Athens, GA 30602-7271, USA
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KEYWORDS VERSION

COMMENT

trimmed to exclude PolyA, vector and regions

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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 TGATGATGTGGGGGTGGTGGCTCATGCGCAGGCGCAGGCGCAGCAGGAGGAGGCGAGAG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 ctcctggagcctggtgccctagaagcccacg 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 GGAGAAGATGCTGGTGTCCGCCATGCCCATG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                      The University of Georgia Plant Sciences Building, I Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                               An EST database from Sorghum: pathogen-induced plants Unpublished (2000)
                                                                                                                                                                                                                                                                         Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sorghum bicolor
Sequences have been
                                                                                                                                                                                                                                    Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 463)
                             Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE600139.1 GI:9855212
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Sequences have been tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _79_G07.b1_A002 Pathogen induced 1 (PI1) Sorghum bicolor cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI: Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptiblity to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be a seedling to the contraction of the clones to be a seedling to the contraction of the clones to be a seedling to the contraction of the clones to be a seedling to the clones to the cl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31.8; DB lu;
Pred. No. 4.2e+02;
""" whatches 37;
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                                                                                                                                                         Athens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                         GA
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                                                                                                                                                         30602-7271, USA
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BE598197/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctcctggagcctggtgccctagaagcccacg 101
                                                                                                                                               Department of Botany
The University of Georgia
Plant Sciences Building, Rm.
                                                               Email: mmpratt@uga.edu
Sequences have been tr
                                                                                                            Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                       clade; Panicoideae; Andropogoneae;
l (bases 1 to 474)
                                                                                                                                                                                                                                                                                                                                                                Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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PI1_66_H03.b1_A002 Pathogen indu
                                          below Phred quality
                                                                                                                                                                                                                        Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                  An EST database from Sorghum:
                                                                                                                                                                                                                                                                                                             Cordonnier-Pratt, M.-M., Gingle, A.,
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primer: JEN REV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptiblity to anthracmose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision. WARRING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from the pathogen."
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/note="Organ: Anthracnose-infected to the very from two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM421 of Collectrichum graminicola, which is a sorghum isolate).
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/db_xref⇔"taxon:4558"
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16. The
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Pred. No. 4.3e+02;
0; Mismatches 37;
                                   to exclude PolyA, vector and regions threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 induced
                                                                                                                                                      2502,
                                                                                                                                                                                                                                                                  pathogen-induced plants
                                                                                                                                                                                                                                                                                                          Dean, R., Sudman, M. and Pratt
                                                                                                                                                    Athens,
                                                                                                                                                                                                                                                                                                                                                            Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA linear EST 18-AUG-2000
d 1 (PI1) Sorghum bicolor cDNA,
                                                                                                                                                    GA 30602-7271,
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BE600794/c
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                                                                                                   Email: mmpratt@uga.edu
Sequences have been tri
below Phred quality 16.
                                                                                                                                                                       The University of Georgia Plant Sciences Building, Rm. Tel: 706 542 1805
                                                                                                                                                                                                                                                                                                      Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                      POLYA-No.
                                                          Seq primer: JEN REV
                                                                                                                                                                                                                                                             Department of Botany
                                                                                                                                                                                                                                                                                  Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                   Cordonnier-Pratt, M.-M., Gingle, A., Dean, R.,
                                                                                                                                                                                                                                                                                                                                                                                            clade; Panicoideae; Andropogoneae;
1 (bases 1 to 487)
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BE600794
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POLYA=No.
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                                        quality sequence stop: 486
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Location/Qualifiers
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/db_xref="taxon:4558"
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59.3%;
                                                                                                      trimmed to exclude PolyA, vector and regions 16. The threshold for highest quality sequence
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Pred. No. 4.3e+02;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487 bp
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bicolor cDNA,
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Bost Local Similarity
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                                                                                                                                                                                  Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                             The University of Georgia Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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1 (bases 1 to 532)
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BE595429
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                                                                                                                                                                                                                                                             Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                           Department of Botany
                                                                                                                                                                                                                                                                                                                                                                               Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
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                                                                                                               quality sequence stop: 525
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1. .532
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1 163 c 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 two-week-old sorghum plants 48 hr after inoculation; vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI: Two-week-old sorghum plants (BTX 623 cultivar) were infected with pathogen (isolate FRM421 of Colletotrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
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/note="Organ: Anthracnose-infected leaves from
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Pred. No. 4.3e+02;
0; Mismatches 37;
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                                                                 Cultivar) were infected with pathogen (isolate FRM421 of Colletotrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptibility to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision. WARNING: while most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from
    the pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      two-week-old sorghum plants 48 hr after inoculation; Vector: pBluescript II from Lambda Zap II; Site_1: X Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Pathogen induced 1 (PI1)"
/note="Organ: Anthracnose-infected leaves from
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DB 10; Length 532; BASE COUNT ORIGIN

Query Match Best Local Matches Local l Similarity 54; Conserv Conservative 31.5%; Score 31.8; DB 10; Pred. No. 4.4e+02; 0; Mismatches 37; Indels 0 Gaps 0

- Вb 103 TGATGATGTGGGGGTGGTGGCTCATGCGCAGGCGCAGGCGCAGCAGAGGAGGAGGAGAA 44
- Qy 71 ctcctggagcctggtgccctagaagcccacg 101
- В GGAGAAGATGCTGGTGTCCGCCATGCCCCATG 13

Search completed: October 3, 2002, 16:14:49 Job time: 16944 sec

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Minimum :
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

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Match Length
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Listing first 45 summaries
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
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3 US-08-658-136-1
1 US-08-451-947-9
2 US-08-421-947-9
3 US-08-928-694-9
5 PCT-US91-06950-9
4 US-09-211-417-2
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Sequence 17, Appli
Sequence 118, App
Sequence 1144, App
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Query Match Best Local S Matches 44

Similarity

27.5%; 62.0%;

Score 27.8; I Pred. No. 10; 0; Mismatches

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Length 722;

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Conservative

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** ** ** ** ** ** ** ** ** ** ** ** **	\$1. \$1. \$1. \$1. \$1. \$1. \$1. \$1. \$1. \$1.		00 0000 0000
ATTORNEY_AGENT INFORMATION: NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 498-8224 TELEPHONE: (617) 498-8224 TELEPHONE: (617) 496-851 INFORMATION FOR SEG ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 722 base pairs TYPE: nucleic acid TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA	TITLE OF NUMBER OO CORRESPO ADDRESS STREET CITY: STATE: COUNTR ZIP: COMPUTER MEDDIM COMPUTER PERAT SOFTWAL CURRENT SOFTWAL CUR	SSULT 1 3-08-702-344-8 Sequence 8, Appleant No. 577 GENERAL INFO GENERAL INFO APPLICANT:	10000000000000000000000000000000000000
TORNEY/ NAME: NAME: REGISTR LECOMMU TELEFAN TELEFAN QUENCE LENGTH: LENGTH: STYPE:	IMBER OF DRRESSON ADDRESS STREET: CITY: CITY: STATE: COUNTRY ZIP: DMPUTER MEDIUM COMPUTER OPERATI OPERATI		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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CLASSIFION: 536 ATTORNEY/AGENT INFORMATION: NAME: Brown, Scott A. REGISTRATION NUMBER: 32, TELECOMMUNICATION INFORMATI TELECHONE: (617) 498-822 TELEFAX: (617) 498-822 TELEFAX: (617) 876-5851 FORMATION FOR SEQ ID NO: 8 SEQUENCE CHARACTERISTICS: LENGTH: 722 base pairs SEQUENCE CHARACTERISTICS: LENGTH: 722 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: LINGAT TOPDLOGY: LINGAT TOPDLOGY: LINGAT TOPDLOGY: LINGAT TOPDLOGY: LINGAT	ENCS:	5 ", F0 A" B	78247 78247 78248 49136 685 685 685 685 685 685 11 1960 1960 2680 2680
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: LENGTH: 6822
: TYPE: DNA
: ORGANISM: HOMO SAPIENS
US-09-426-998-3
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; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Query Match
Best Local Similarity
                                                                                                                                           SOFTWARE: PATENTIN VER. 2.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09426998 Patent No. 6358706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, John SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: THEBERCULOSIS
TITLE OF INVENTION: THEBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT ENLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/426,998
CURRENT FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                            APPLICANT: DUBIN, ADRIENNE E.
APPLICANT: PYATI, JAYASHREE
APPLICANT: ZHU, JESSICA Y
APPLICANT: ETLANDER, MARK G
APPLICANT: GALLNDO, JOSE E
TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
TITLE OF INVENTION: CHANNEL (ALPHAIG-C)
FILE REFERENCE: ORT-1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11849 aggccccaccgtgtgacgaccggcctcaggagcgcggttgcacctcgacgctcggtggtc 11908
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27.3%;
56.7%;
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Score 27.6;
Pred. No. 14;
            DB 4;
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            Length 6822;
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; SEQ ID NO 4
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Patent No. 5654170
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GALINDO, JOSE E TITLE OF INVENTION: DAM ENCODING HUMAN ALPHAIG T-TYPE CALCIUM TITLE OF INVENTION: CHANNEL (ALPHAIG-C) FILE REFERENCE: ORT-1057
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CURRENT FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VER. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DUBIN, ADRIENNE E. APPLICANT: PYATI, JAYASHREE APPLICANT: ZHU, JESSICA Y
                                                                                                         APPLICAMY: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
MUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                        APPLICANT: K
APPLICANT: L
APPLICANT: B
APPLICANT: C
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
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                                                                                  COUNTRY:
                                                                                               CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 ggggagtcctcctggagcctggtgccctag 92
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                                                                                    USA
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                                                                                                                                                                                                                           DACKOWSKI, WILLIAM GERMINO, GREGORY
                                                                                                                                                                                                                                                        CONNORS, TIMOTHY D
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                                                                                                                                                                                                                                                                                                       KLINGER, KATHERINE W.
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Pred. No. 15;
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Best Local Similarity
Matches 47; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31571 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16488 TGAGGCCTCCGGGTCCTGGG 16507
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,8
                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                   ADDRESSEE: GENZYME CORPORATION STREET: ONE MOUNTAIN ROAD CITY: FRAMINGHAM
                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 12-OCT
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GERMINO, GREGORY
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ELIZABETH
JMBER: 31,845
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58.8%;
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Pred. No. 22;
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RESULT 7
US-08-658-136-1
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                                                                          TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
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STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: 1
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN
                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                     SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
TYPE: nucleic acid
                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
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LENGTH: 53526 base pairs
TYPE: nucleic acid
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                                                                               TELEPHONE: 508-072-5415
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                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                         CITY: FRAMINGHAM
STATE: MASSACHUS
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47; Conserv
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LANDES, GREGORY
               linear
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                                                                                                         508-872-8400
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  DNA (genomic)
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Pred. No. 23;
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                        Query Match
Best Local Similarity
"---hes 49; Conserv?
                                                                                                                       US-08-451-947-9
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US-08-451-947-9/c
Sequence 9, Application US/08451947
Patent No. 5702906
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Best Local Similarity 58.8%;
Matches 47; Conservative
                                                                                                                                                                                            TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                          TYPE: nucrease sing STRANDEDNESS: sing
                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMER: 08/426419
FILING DATE: 19-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICANT: ROSENTHAL, ARNON
NAME: Torchia, Timothy E. REGISTRATION NUMBER: 36,700 REFERENCE/DOCKET NUMBER: 66
                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                             1190 bases
                                       Conservative
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                                                    26.5%;
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                                    Score 26.8; DI
Pred. No. 20;
0; Mismatches
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Pred. No. 23;
0; Mismatches
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                                                                Length 1190;
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RESULT 10
US-08-928-694-9/c
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Best Local (
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                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
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APPLICATION NUMBER: 07/587707
FILING DATE: 25-5EP-1990
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/240387
FILING DATE: 10-May-1994
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SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
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ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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                                                                                                                       469 TGTCGAGGATGGGGTTAGGACTCCAATGACACACTGGGGAGGAGGAAAATGAGGGGGATG 410
                                                               409 CGGAGGGAGCCTGGGGGAGCAGGAGC 384
                                                                               71 ctcctggagcctggtgccctagaagc 96
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                                                                                                                                                                                                                                                                                                         TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/6 FILING DATE: 31-JAN-1991
                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Torchia, PhD., Timoth
REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/424,826A FILING DATE: 19-Apr-1995 CLASSIFICATION: 514
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Pred. No. 20;
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RESULT 11
PCT-US91.06950-9/c
; Sequence 9, Application PC/TUS9106950
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GENERAL INFORMATION:
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Best Local Similarity
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                  APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/451947
FILING DATE: 26-MAY-1995
PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5 Inch, 1.44 Mb |
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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NUMBER OF SEQUENCES:
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                                                                                                                                                                        71 ctcctggagcctggtgccctagaagc 96
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Nucleic Acid
STRANDEDNESS: Single
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REGISTRATION NUMBER: 36,700
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             GENENTECH, INC. ROSENTHAL, ARNON
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NOVEL NEUROTROPHIC FACTOR
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Pred. No. 20;
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Best Local Similarity
Watches 49; Conserve
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                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: RAITHER, Jerome B
APPLICANT: Whitehead, Clark M
TITLE OF INVENTION: NUCLEOLUS AUTOANTIGENIC MARKER FOR SYSTEMIC LUPUS
TITLE OF INVENTION: ERHYEMATOSUS
TITLE OF INVENTION: GenBank
TITLE OF INVENTION: Accession Number U86751
                                                              SEQ ID NO 2
LENGTH: 3286
                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09211417A Patent No. 6177254
                                                                                                                               CURRENT APPLICATION NUMBER: US/09/211,417A CURRENT FILING DATE: 1998-12-15
                                                                                                NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver.
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
OTHER INFORMATION: Nucleic Acid Sequence of ASE-1
                 FEATURE:
                             ORGANISM: Homo sapiens
                                                  TYPE: DNA
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PRIOR APPLICATION NUMBER: 07/648482
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MEDIUM TYPE: 5.25 in
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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CITY: South San Francisco
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                                                                                                 Ver. 2.0
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57.0%;
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Pred. No. 20;
0; Mismatches
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APPLICANT: Magna, Holly
APPLICANT: Schaffer, Paul
APPLICANT: Lawton, Michael
APPLICANT: Lawton, Michael
APPLICANT: Yocum, Sue
APPLICANT: Mitchell, Peter
APPLICANT: Mitchell, Peter
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN NUCLEOTIDE PYROPHOSPHOHYDROLASE-2
FILE REFERENCE: PF-0420 US
CURRENT APPLICATION NUMBER: US/08/996,083A
CURRENT FILING DATE: 1997-12-22
NUMBER OF SED ID NOS: 3
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US-09-429-516-2
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Best Local Similarity 57.0
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6177254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: Incyte Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                            CORRESPONDENCE ADDRESS
                                                 APPLICANT: Hutchinson, Nancy
APPLICANT: MUTTY, Lynn E.
TITLE OF INVENTION: HUMAN NUCLEOTIDE PYROPHOS
TITLE OF INVENTION: PHOHYDROLASE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 4183
                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                        636 gtgtccagggtgcagccttgacacct 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               840 GGATCCTTAGGGTGCCCTGGGGGGCTGAGGCACAGGTGAGTCCACCTCCTGCCT 787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                       l Similarity
37; Conserv
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3174 Porter Drive
                                                                                                              Mitchell, Peter
                                                                                                                                                       Schaffer, Paul
                                                                                                                          Lawton, Michael
Yocum, Sue
                                                                                                                                                                        Magna, Holly
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57.0%;
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Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
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US-08-290-665A-140/c

; Sequence 140, Application US/08290665A

; Patent No. 5882852
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; LIBRARY: SATPE
; CLONE: 1388013
US-09-429-516-2
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Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
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                                                                                                                                                                TITLE OF INVENTION:
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ZIP: 10154
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN &
                                                                                                                                                                                                                                                       APPLICANT: BUKH, J., APPLICANT: PURCELL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 4183 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                               636
                                                                                                                                                                                                                                                                                                                                                                                                                                                           576
                                                                                           STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK
                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                               65 ggagtcctcctggagcctggtgccct 90
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OPERATING SYSTEM:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINE
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for Windows Version
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Pred. No. 23;
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ATTORNEY/AGENT INFORMATION:

NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 226-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: 28
US-08-290-665A-140
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Search completed: October 3, 2002, 16:21:45 Job time: 16945 sec
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Hest Local Similarity 56.2%; Pred. No. 21;
Matches 50; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION USER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
TECHNOLOGY
                                                                                                                                             299 GGGGACAGGAGCCAACCTGCCCACCACA 271
                                                                                                   65 ggagtcctcctggagcctggtgccctaga 93
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Listing first 45 summaries
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1172.8
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1: /SIDSI/gcgdata/gc22: /SIDSI/gcgdata/gc33: /SIDSI/gcgdata/gc44: /SIDSI/gcgdata/gc5: /SIDSI/gcgdata/gc5: /SIDSI/gcgdata/gc6: /SIDSI/gcgdata/gc9: /SIDSI/gcgdata/gc9: /SIDSI/gcgdata/gc9: /SIDSI/gcgdata/gc9: /SIDSI/gcgdata/lc1: /SIDSI/gcgdata/lc1: /SIDSI/gcgdata/lc1: /SIDSI/gcgdata/lc1: /SIDSI/gcgdata/lc1: /SIDSI/gcgdata/lc2: /SIDSI/gcgdata/lc3: /
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| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
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Human AMPK gamma s
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Pig AMPK gamma sub
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Human pancreatic
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			5555577	23.7 22.3 22.3 18.2 16.9 15.3 15.3 15.3 15.3 15.3
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ALIGNMENTS

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Homo sapiens

PRKAG3 cDNA

21-JAN-2002 AAH43685;

Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.

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(AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders suc as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.
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Matches Query Match Best Local

cal Similarity 97. 1495; Conservative

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Score 1447; D Pred. No. 0; 0; Mismatches

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                                                                              cc useful as therapeutic for treating carbohydrate metabolism disorders such cas diabetes, obesity, and disorders associated with muscle metabolism cc such as myopathy and cardiovascular diseases, to modulate AMPK cc activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic cevaluation, genetic testing and prognosis of a metabolic disorder. Cc evaluation, genetic testing and prognosis of a metabolic disorder. Cc evaluation, genetic testing and prognosis of a metabolic disorder. Cc evaluation of carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are cc useful for detecting a dysfunction of carbohydrate metabolism resulting cf rom the expression of a functionally altered allele of PRKAG3.

Cc Transgenic animal and host cell transformed with PRKAG3 or a creening compounds able to modulate AMPK activity. Nucleic acid cencoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of pressure and a sequence encoding the first cystathione beta synthase
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Sequence
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The present sequence is pig adenosine monophosphate (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic

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CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, CC PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.
CC Mutation in Prkag3 results in an altered regulation of carbohydrate CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as CC therapeutic for treating carbohydrate metabolism disorders such as CC diabetes, obseity, and disorders associated with muscle metabolism CC such as myopathy and cardiovascular diseases, to modulate AMPK CC activity, and for restoring a normal AMPK function. PRKAG3 sequence CC and its functionally altered mutants are useful for the diagnostic CC referably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are CC useful for detecting a dysfunction of carbohydrate metabolism resulting CC from the expression of a functionally altered allele of PRKAG3. CC Transgenic animal and host cell transformed with PRKAG3 or a carbohydrate animal and host cell transformed with PRKAG3 or a conding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain CC of PRKAG3 and is useful in gene therapy.

밁 δ 늉 Ŷ В Ş

Sequence 1867 ВP; 380 A; 583 C; 529 G; 375 T; 0 other;

Similarity

68.9%;

DВ

22;

Length

1867;

δÃ 밁 Ş Ъ Ş 밁 Q Š В 밁 δδ 밁 Š 밁 Qy 밁 γQ В Ş В ş Query Match Best Local Sim Matches 1309; 598 869 538 638 478 418 518 361 458 301 398 338 241 101 281 121 221 161 181 61 <u>بــ</u> gcccctctatgggacagcaagaagcagagctttgtgggggatgctgaccatcactgacttc gcacctttgtgggacagcaagaagcagagcttcgtggggatgctgaccatcacagacttc gacaccatgctggagatcaagaaggccttctttgctctggtggccaacggtgtgcgggca ttcatgcaggagcacacctgctacgatgccatggcaactagctccaagctagtcatcttc tttcccaagctgggctgggatgacgaactgcggaaaccccggcgcccagatctacatgcgc gatgagct---tgggctggtggaagagaagccagcccgtgcccatccccagaggtgctg tytgagctagaaggcctgctggaagaggcctgccctgtgcctgtccccgcaggcccca ggctccagcacagatgatgtggagctggccacggagttcccagccacagaggcctgggag agaatccgtgggaaacggagggccaaagccttgagatggacaaggcagaagtcggtggag gacaccatgctggagatcaagaaggccttctttgccctggtggccaacggcgtccgagcg ttcatgcaggagcacacctgctacgatgccatggcgaccagctccaaactggtcatcttc ttacccaggctgggctgggatgatgagctgcagaagccgggggcccaggtctacatgcac gactccaacacagaccatctggatctgggcatagagttctcagcctcggcggcgtcgggg gtggacaacccccaacagagcgggacatcctcccctctgactgtgcagcctcagcctcc gtgggcactccaccaagggtgggactgcctcccctctgactgtacagcctcagctgca gggcaggaggccacattccccaaggccacacccttggcccaagccgctcccttggccgag gaaggggggcctccggggcccgagggaaggtccccagtccaggccagttgctgagtccacc gaaggggagccaccaggtcagggggaaggtccccggtccaggccagctgctgagtccacc agaagccatggggaccaggggaacaaggcctctagatggacaaggcaggaggatgtagag ttcctagagcaaggagagccgttcatggccatcccgagctgtaaccaccagctcagaa Conservative 0 Score 1134.4; I Pred. No. 4.1e-: 0; Mismatches Indels ., Gaps 657 757 537 637 577 517 457 180 120 220 477 417 360 300 397 240 337 60 4.

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RESULT
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proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; inhibin; chemotaxis; chemokinesis; vulnerary; antiulcer; thrombolysis; oncogenesis;

WO200157188-A2

09-AUG-2001

05-FEB-2001; 2001WO-US03800

03-FEB-2000; 27-APR-2000; 2000US-0496914 2000US-0560875

(HYSE-) HYSEQ INC

Tang Liu c, Drmanac

2001-457740/49 DB; ABB11241.

Claim 1; Page 429; 1963pp; English

cc haematopoles is regulatory activity; tissue growth activity; chammatopoles is regulatory activity; activity inhibin related activities; chammatopoles is regulatory activity; activities; haemostatic, thrombotic or chemokinetic activities; haemostatic, thrombotic or chemokinetic activities; haemostatic, thrombotic or chemokinetic activities; haemostation or may be converted in oncogenesis, cancer cell proliferation or metastasis.

Cc Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g.,myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions include cancers, chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal coropair (or nucleic acids encoding them) may be used to promote wound chealing (e.g., of burns, incisions and ulcers), while those with conditions of the conditions of manune disorders. sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cycokine, cell proliferation or cell differentiation activities, stem cell growth factor activity; Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention. tides of medical

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metabolic disease; diabetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and me for determining a risk estimate of diseases in subject by detecting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated 5'-AMP-activated protein kinase subunit(s) - us develop products for treating e.g. hyper-cholesterolaemia, o hypoxia, ischaemia, nutrition disorders or diabetes mellitus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arteriosclerosis; bronchitis; emphysema; hypereosinophilia; myocardial inflammation; pericardial inflammation; anaemia; rheumatoid arthritis; Addison's disease; AIDS; atherosclerosis;
WPI; 1999-080952/07
                                                                                                             (INCY-) INCYTE PHARM INC
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alignments, and a consensus sequence was derived from the extended CC and overlapping Incyte clones 3075712/HEARNOTO1, 842220/PROSTUTO5, CC 1364747/SCORNONO2, 145972 and 145802/PRNITUTO1 and 1479332/CORNOTO2. CC DAPK-7 shows 73% homology with the human foetal liver AMPK gamma CC subunit (GI 1335856), and is associated with cDNA libraries which CC are immortalised or cancerous and show inflammatory or immune CC responses. The invention provides disease associated protein kinases CC DAPK-1 to DAPK-7 (see AAWB8412-38) and cDNA clones encoding them (see CC AAXO6331-36 and AAXO6682), as well as expression vectors, host cells, CC uses of such products in the diagnosis, prevention and treatment of CC disease associated with cell proliferation, especially cancer or an adult respiratory distress syndrome, allergies, asthma.
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Best Local Similarity 62.9
Matches 567; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adult respiratory distress syndrome, allergies, asthma, arteriosclerosis, bronchitis, emphysema, hypereosinophilia, myocardial or pericardial inflammation, rheumatoid arthritis.
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liferation and to treat the immune response an
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                                                                Ota T,
Ishii :
         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection
                                                                                                                                                                                                                                   EP1074617-A2
                                                                                                                                                                                                                                                                                                      Human cDNA sequence
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Nagai K,
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Otsuki
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cc full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary cc to the complementary strand of a polynucleotide which comprises one of ct the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination cc of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination cc complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a cc polynucleotide which comprises a 3'-end sequence, where the cc oligonucleotide which comprises a 3'-end sequence, where the cc oligonucleotide comprises a 3'-end sequence, where the cc the 5'-end sequence/3'-end sequence is selected from those defined in cc the specification. The primers are useful for synthesising polynucleotides, cc particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by ct the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB13633 to AAH18742 represent human cDNA sequences; aAB92446 to CC AAB95893 represent human cDNA sequences; aAAB9246 to CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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genes from Drosophila
interactions -
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RESULT
AAH43684
                The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6.
                                                                                                                                                                             New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and for determining a risk estimate of diseases in subject by detectivariant.
                                                                                                                                                         Example 1;
                                                                                                                                                                                                                                                    Andersson
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obesity; substitution; 
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Best Local Similarity 97.6%;
Matches 283; Conservative
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24-FEB-2000
02-MAR-2000
11-MAR-2000
11-MAR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
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2000US-0198974
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2000US-0205515
2000US-0216486
2000US-0216486
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useful for metastasis Nucleic acids encoding preventing, human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and $% \left(1\right) =\left(1\right) \left(1\right)$

WPI;

2001-483426/52

Rosen

CA,

Barash

SC,

Ruben

MS

Disclosure; SEQ ID NO 27552; 3071pp + Sequence Listing; English

CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) CC amino acid sequences given in AAM62170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK64950 and AAM62169 crepresent sequences used in the exemplification of the present invention.

Sequence 3425 BP; 916 A; 794 ე: 951 G; 764 ·-0 other;

15.3%; Score 252; DВ 22; Length 3425;

Query Match

멍 Ş Вþ Qy Ъ Qy B Qy B Ş Matches 252; Conser 3185 1636 3245 1576 3305 3365 1456 3425 1396 1516 CACCTGCACACCTGGAAGCCAATGAAGGGAACTGGAGAACTCAGCCTTCATCTTCCCCCA ctcttagtcttc CCCCCATTTGCTGGTTCAGCTATGATTCAGGTAGGCTCTGCCCTGGGCCATGACACCAGC CTCTTAGTCTTC Conservative 1647 3174 0 Pred. No. 1.3e-55; Mismatches 0; Indels 0: Gaps 3186 1635 1575 3246

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ALIGNMENTS

o Car	FEATURES	JOURNAL	AUTHORS	ORGANISM REFERENCE	RESULT 1 B1344527 LOCUS DEFINITION ACCESSION VERSION VERSION
/organism="Sus scrofa" /db_xref="taxon:9823" /clone_lib="MARC 2PIG" /tissue_type="pooled" /lab_host="DH10B" /note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI;	POR PRIMER'S PORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTACGACG Plate: 119 row: I column: 11 Seq primer: ATTTAGGTGACACTATAG. Location/Qualifiers	EST discovery in swine Unpublished (2000) Contact: Smith TPL	eking,B.A., Rohrer,G.A., Smith,T.P.L., Cas M.P., Grosse,W.M., Bennett,G.A., Laegreid,	pig. pig. Sus scrofa Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 572)	BI344527 572 bp mRNA linear EST 30-JUL-2001 373008 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence. BI344527 BI344527.1 GI:15037807

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JOURNAL COMMENT
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              Li.W.B., Gruber,C., Jessee,J. and Polayes, Full-length cDNA libraries and normalizati Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.Location/Qualifiers
                                                                                           Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 970)
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No. 4.6e-97;
                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                         normalization
                      Web : www.genoscope.cns.fr.
                                                                                  Polayes, D.
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/clone_lib="LTI_FL015_Brn1"
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20568495
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Cellular Immunology
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,J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs
analysis of vertebrate gene function
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html
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/strain="CB"
/db_xref="taxon:9031"
/clone="25f16r1"
/clone_lib="dkfz426"
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It,
N., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuu
                                                                                                                                                                                                                                                                                                     Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
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                                        Watahiki,M., Yoneda,Y., Isl
,S., Kawai,J., Okazaki,Y.,
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BB630381 RTKEN full-length enriched, 6 days neonate
musculus cDNA clone A030014A04 5', mRNA sequence.
BB630381
                           Hayashizaki,Y.
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RIKEN integrated sequence analysis (RISA) system -- 384 - format
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                                                               Tanaka,T., Matsuura
                                                                                                                                                                                                                                                                                                     (RIKEN)
awa 230-0045, Japan
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                                                                                                                                                                                   TGGCCCTCACCAGCTGTGGCCACCAGCTCAGAAAGAACCTGTGCCATACGGGGAGTCAAG 177
                                                                                                                                                                                                                                                                                                           GGAGCTGGCCGCATGGAGCCCGAGCTGGAGCACACTTGCCTGGGACCCTGACCTGGAGC
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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,Y. and Hayashizaki,Y.
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/dev_stage="6 days neonate"
/lab_host="DH10B"
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/clone_lib="RIKEN full-length enriched,
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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1 (bases 1 to 921)
Li,W.B., Gruber,C.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/tissue_type="placenta"
/tissue_type="placenta"
/note="wector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA
/note="wector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSPORT 6
vector. Library was normalized. Library was constructed by
vector fibrary was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                       http://fulllength.invitrogen.com"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.
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/db_xref="taxon:9606"
/clone="csODKOO7yE02"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
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                                                  AGCTAGAAGAACACAAGATAGAAACTTGGAGAGAGGTGTATCTCCAGGACTCCTTTAAAC
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/note="Yector: pCMVSPORT 6; NotI; 1st strand constructed by Life Technologies, Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
/note PCMVIIle, Maryland 20850, USA Fax: (1) 301 610 8371
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467815 MA
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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                  Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.1 Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C. Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
                   BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: I column: 16
Seq primer: ATTTAGGTGACACTATAG
                                                                                                              and -minmatch 12
PCR PRimers
                                                                                                                                                                                                                             Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                            Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                           FORWARD: AGGAAACAGCTATGACCAT
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Location/Qualifiers
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                                                                                            prime, mRNA
AL552459
AL552459.1
     Eukaryota: Metazoa: Chordata: Mammalia: Eutheria: Primates: 1 (bases 1 to 908)
Li,W.B., Gruber,C., Jessee,J.
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AL552459 LTI_NFL006_PL2
                                                       Homo sapiens
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/ob_xref-"taxon:9913"
/clone_lib-"MARC 2BOV"
/tissue_type-"pooled"
/lab_host="DH10H"
                                                                                                                                                                                                               548
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                                                                                             GI:12891378
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No. 6.le-73;
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                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                     GCACTACCACCCCCGTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCC
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                                                                                        TCATGTCCAAGTCTCTGGAAGAGCTACAGATTGGCACCTATGCCAATATTGCTATGGTTC
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Full-length cDNA libraries Unpublished (2001) Contact: Genoscope
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/clone="CS0D1070YC03"
/tissue_type="placenta"
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/note="Vector for intervent inte
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Contact: Genoscope
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//tissue_type="neuroblastoma cells"
//tissue_type="neuroblastoma cells"
//lab_nost="DH10B"
//note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
//note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
//note="Organ: brain; Vector: pcmVSPORT 6; 1st strand cDNA
//note="Organ: brain; Vector: Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library is not normalized, but is the control for
the normalized libraries. Library was constructed by Life
Technologies. Contact: Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
// Maryland 20850, USA Fax: (1) 301 610 8371 Email:
fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
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Contact: Genoscope
Genoscope - Centre National de Sequencage
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BP 191 91006 EVRY cedex - France
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1 (bases 1 to 951)
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nilarity 62.7%;
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/clone_ib="LTI_NFL006_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: pCMVSpORT 6; Site_1: Not1; 1st strand cDNA
/note="Vector: pCMVSpORT 6; Site_1: Not1; 1st strand cDNA
was primed with a Not1-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
bttp://filllenia.cd.
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AGENCOURT_6427350 NIH_MGC_72
5', mRNA sequence.
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BM462694.1 GI:18511734
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:5540312"
/clone="Lib="NIH_MGC.72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="organ: skin; Vector: pcMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo (Average insert size 2 kb. Library constructed by Life
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AGENCOURT_6476961 NIH_MGC_85
5', mRNA sequence.
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                                                                                            cacacaaacgcctgctcaagttcctgcacatctttggttccctgctgccccggccctcct 1046
                                                                                                                                                                        accggatccatcgcctgttcttgacccggtgtcaggcaacgtactccacatcctca 986
                                                                                                                                                                                                                                                ctctggtctccatctctcclaatgatagcctgtttgaagctgtctacaccctcatcaaga 926
                                                                                                                                                                                                                                                                                                                            agattgaacaacataagattgagacctggaggggagatctacctgcaaggctgcttcaagc
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Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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(bases 1 to 1004)
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//db_xrefe="taxon:9606"
//db_xrefe="taxon:9606"
//clone=="IMAGE:5553194"
//clone=_IIb="NIH_MGC_85"
//tlssue_type="lymphoma, cell line"
//lab_host="DH10B (phage-resistant)"
//lab_host="DH10B (phage-resistant)"
//note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
54 a 247 c 232 g 265 t 6 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cogburn, L.A. and Monsonego-Ornan, E.
ESTs from Normalized Chicken Breast Muscle, Leg Muscle,
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal
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302-831-2822
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                                                                                                                    /note="Vector: pcMvSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"

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Version

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Sequence 14, Application US/08878989
Patent No. 5885803
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hilman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Lal, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      Matches 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: line IMMEDIATE SOURCE:
                                                                                                                      423
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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NUMBER OF SEQUENCES:
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STREET: 3174 Por
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: PENITUT01
CLONE: 1452972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: sing
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TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/878,989 FILING DATE:
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                accggatccatcgcctgcctgttcttgacccggtgtcaggcaacgtactccacatcctca
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                                                                      ctctggtctccatctctcctaatgatagcctgtttgaagctgtctacacccctcatcaaga
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US-09-272-796-14
                                                          STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION: NUMBER: US/09/272,796
FILING DATE:
CLASSIFICATION: DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
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APPLICANT: Hillman, Jennifer L
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
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ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J J
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CORRESPONDENCE ADDRESS:
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                                                    FILING DATE:
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Query Match 22.3%;
Best Local Similarity 62.9%;
Matches 567; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PENITUTO1
CLONE: 1452972
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REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
                                       agaggacactatgtctggagggagtcctttcctgccagccccacgagagcttgggggaag 1346
                                                                                                               acctggctgcccagcaacctacaaccacctggacatgagtgtgggagaagccctgaggc 1286
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Pred. No. 2.8e-87;
0; Mismatches 334;
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMTELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                             1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
924 agaaccggatccatcgcctgcctgttcttgacccggtgtcaggcaacgtactccacatcc 983
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                                                                                                                  y Match 3.0%; So
Local Similarity 2.6%; Pro
hes 10; Conservative 220;
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                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                   agcctctggtctccatctccctaatgatagcctgtttgaagctgtctacaccctcatca 923
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                                                                                                                                Score 49; DB 1; Length 7218; Pred. No. 0.0021;
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                                                                                                              Mismatches 155; Indels
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LENGTH: 1022
TYPE: DNA
ORGANISM: Homo sapiens
US-09-056-105-8
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; Sequence 8, Application US/09056105

; Patent No. 6287569
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APPLICANT: KIPPS, TH
APPLICANT: WU, YUNQI
                                                                                                                                                                                                                                                                                                                                                                                             Matches 160;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR TITLE OF INVENTION: PROCESSING FILE REFERENCE: 233/221
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                                                                                                                                       acccggcgcccagatctacatgcgcttcatgcaggagcacacctgctacgatgccatggc 612
                                                                   aactagctccaagctagtcatcttcgacaccatgctggagatcaagaaggccttctttgc
                                                cctgaagatgatctttggcattgacgtgaaggaagtggaccccgccagcaacacctacac
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Pred. No. 0.12;
0; Mismatches 198; Indels 0
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 4.5%
Matches 12; Conservative
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                                                                                                  1187
                     1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                          1247
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APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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TELEFAX: (703)683-4109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500
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                                                                                                                                                                                                                                           gccttgagatggacaaggcagaagtcggtggaggaagggagccaccaggtcagggggaa 247
                                                                                            agccttgggggttctgagcatcaagaqatgagcttcctagagcaagaaaacagcagctca 127
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                                                                                                                                                                    ccttgtcacctgcctgggcctttcctatgatggcctgctgggtaataatcagatcttt 656
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SYSTEM: PC-DOS/MS-DOS
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4.5%; Pred. No. 0.44;
/ative 150; Mismatches 103;
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                                                                                                                                                                                                                                         Sequence 14,
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Best Local Similarity
Matches 159; Conserv
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APPLICANT: WU, YUNQI
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: PROCESSING
TITLE OF INVENTION: PROCESSING
TITLE OF INVENTION: PROCESSING
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
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                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                     APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry; APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De APPLICANT: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules | TITLE OF INVENTION: Determining Expression Of A Tumo
                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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STREET:
CITY: N
STATE:
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                                                    ADDRESSEE:
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                                                                                                                                                                                                                       4, Application US/08299849B 5612201
             SEE: Felfe & Lynch
: 805 Third Avenue
New York City
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                                                                                                       Isolated Nucleic Acid Molecules Useful In Determining Expression Of A Tumor Antigen
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Pred. No. 0.31;
""smatches 199;
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Length 1022; Indels

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Best Local Similarity 44.4%;
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 838-388
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                  1098 CCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCACCAGCAACACCCTACAC 1157
                                                                                                                       1038 GAGAGTCATCAAAAATTACAAGCGCTGCTTTCCTGTGATCTTCGGCAAAGCCTCCGAGTC 1097
673 totggtggccaacggtgtgcgggcagccctctatgggacagcaagaagcagagcttt 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: FEATURE:
                                                                                  613 aactageteeaagetagteatettegaeaeeatgetggagateaagaaggeettettege 672
                                                                                                                                                                                                        978
                                                                                                                                                                                                                   493 cctgtgcctgtccccgcaggccccatttcccaagctgggctgggatgacgaactgcggaa 552
                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                              553 acccggcgcccagatctacatgcgcttcatgcaggagcacacctgctacgatgccatggc 612
                                                                                                                                                                                                                                                                    918 CTCGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGC
                                                                                                                                                                                                                                                                                          433 gttcccagccacagaggcctgggagtgtgagctagaaggcctgctgggaagagggcctgc 492
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APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleion STRANDEDNESS: TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hanson, No. 5612201man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/764,364 FILING DATE: 23-SEPTEMBER-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/299,849B
FILING DATE: 1-SEPTEMBER-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                             TCATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGA 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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9-JULY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 199; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39.6; DB Pred. No. 0.43;
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                                                                                                                                             Matches 159;
                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 838-38
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                      TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5925729man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
APPLICATION NUMBER:
PRIOR APPLICATION DATA:
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SOFTWARE: WORDERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
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LENGTH: 2531 base pairs
433 gttcccagccacagaggcctgggagtgtgagctagaaggcctgctgctgcagaagagaggcctgc 492
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PRIOR APPLICATION NIMBER: 07/764,364
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry; AppLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, El APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, (TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor TITLE OF INVENTION: Rejection Antigens and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1158 CCTTGTCACCTGCCTGGGCCTTTCCTATGATGGCCTGCTGGGTAATAATCAGATCTTT 1215
                                                         858 CACTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAAGAGGAGGGGCCAAGCAC 917
                                                                                 373 ctctgactgtacagcctcagctgcaggctccagcacagatgatgtggagctgggcacgga 432
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                                                                                                                                         y Match 2.4%;
Local Similarity 44.4%;
hes 159; Conservative
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                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/705,702 FILING DATE: 23-May-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 02-MAY
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                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (212) 838-3884
                                                                                                                                                                                                                                                           MAGE-41 gene
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12-DECEMBER-1991
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22-MAY-1992
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9-JULY-1991
                                                                                                                                             0;
                                                                                                                                                           Score 39.6; DB 2;
Pred. No. 0.43;
                                                                                                                                           Mismatches
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US-08-967-727-14
                                                                                                         APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 6025474man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6025474
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14,
                                                                        TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 0:
FILING DATE: 12-DECEMPRIOR APPLICATION DATA:
APPLICATION NUMBER: 0:
FILING DATE: 23-SEPTER
                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/7:
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US92/04
FILING DATE: 22-MAY-1992
PRIOR APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
  LENGTH: 22-
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 805 Third AVCITY: New York City
STATE: New York
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acccggcgcccagatctacatgcgcttcatgcaggagcacacctgctacgatgccatggc 612
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                                   2531 base pairs
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23-SEPTEMBER-1991
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                                                                                                                                                       LUD 5353
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US-08-967-727-14
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Patent No. 6
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Matches
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                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
                                                                                                                                                                                                                                                                         COMPUTER: IBM
OPERATING SYSTEM: PC-DC
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 A
                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1158 CCTTGTCACCTGCCTGGGCCTTTCCTATGATGGCCTGCTGGGTAATAATCAGATCTTT 1215
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                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 26-MAF CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 805 Third Avenue CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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mes 159; Conserv
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                                                                                                                                                                                                                                        26-MARCH-1993
                                                                                                                                                                                                                                                                                                                                                          Diskette, 5.25
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FILING DATE: 23-MAY-1991 ATTORNEY/AGENT INFORMATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

07/705,702

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APPLICANT: KIPPS, THOMAS J.
APPLICANT: WJ, YUNOI
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT APPLICATION UNMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                             US-09-056-105-10
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                                                                                                                                                                                                                                                                                                                  Sequence 10, Applica Patent No. 6287569 GENERAL INFORMATION:
                                                                            SOFTWARE: FASTSEQ
SEQ ID NO 10
LENGTH: 4895
TYPE: DNA
ORGANISM: Homo sapiens
-09-056-105-10
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INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 2531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local
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REFERENCE/DOCKET NUMBER: LUI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1038 GAGAGTCATCAAAAATTACAAGCGCTGCTTTCCTGTGATCTTCGGCAAAGCCTCCGAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             613 aactagctccaagctagtcatcttcgacaccatgctggagatcaagaaggccttctttgc 672
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Local Similarity 44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCACCAGCAACACCTACAC 1157
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; LOCATION: (1)...(289)
; OTHER INFORMATION: n =
US-09-007-005-17
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                                                                                                                                                                         Query Match
Best Local
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
CARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 159; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 28
TYPE: RNA
                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
186 NYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSY 127
                               954 acccggtgtcaggcaacgtactccacatcctcacacacaacgcctgctcaagttcctgc 1013
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                                                                     GYAYGYTYTAYCYGYCYAYGYCYTYGYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSY 187
                                                                                                                                                       al Similarity
10; Conserv
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                                                                                                                                               Pred. No. 0.31;
87; Mismatches
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APPLICANT: SZOSTAK, Jack W.
APPLICANT: ROBERTS, KICHARD W.
APPLICANT: L1U, Rihe
TITLE OF INVENTION: ESLECTION OF PROTEINS USING RNA
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
CURRENT APPLICATION UNUMBER: 05/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EEARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
EEARLIER APPLICATION NUMBER: 05/064,491
EEARLIER APPLICATION NUMBER: 09/007,005
EEARLIER APPLICATION NUMBER: 09/007,005
EEARLIER APPLICATION NUMBER: 09/007,005
EEARLIER APPLICATION NUMBER: 05-007,005
EEARLIER APPLICATION NUMBER: 05-007,00
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US-09-404-650-1
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: LOCATION: (1)...(289)
: OTHER INFORMATION: n = A,T,C
US-09-244-796-17
Sequence 1, Application US/09404650
Patent NO. 6309858
GENERAL INFORMATION:
APPLICANT: Dietrich, Paul S.
APPLICANT: McGivern, Joseph G.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
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Best Local Similarity 5.3%; Pred. No. 0.31;
Matches 10; Conservative 87; Mismatches
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; LOCATION: (192)..(6716)
US-09-404-650-1
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Best Local Similarity 47.5%;
Matches 115; Conservative
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FILE REFERENCE: RO043B-REG sequence listing
CURRENT APPLICATION NUMBER: US/09/404,650
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                   4349 tgtgctcaacatgtftgtgggtgtcgtggtggagaacttccacaagtgccggcagcacca 4408
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Search completed: October 3, 2002, 16:22:08 Job time: 16968 sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                   Score
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                                    Description
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AX281582
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DEFINITION
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Sequence 5 from Patent W00177305.
AX281582
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                         Arexis AB (SE)
                                                                                                                                                                                                                  Andersson, L., Luthman, H. and Marklund, S. Variants of the human amp-activated protein kinase gamma 3 subunit Patent: WO 0177305-A 5 18-OCT-2001;
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20. .1489
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AX090314 Homo sapi
AX093564 Homo sapi
AX093564 Homo sapi
AX0935677 Homo sapi
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PAT 02-NOV-2001

Result No.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. Characterization of AMP-activated protein kinase isoforms and their role in AMP binding Biochem. J. 346 Pt 3, 659-669 (2000) 20164049
                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-OCT-1999) Carling D., Co
Clinical Sciences Centre, Hammersmith
London, W12 ONN, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens mRNA for AMP-activated (AMPK gamma 3 gene). AJ249977
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LQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNUHILTHKRLKAFLHF
GGSLLPRSBETYRFIODALGTFREADAVLETAEDITALDIFVDRRVSALVENGVNGVCGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNUHILTHKRLKELHF
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LVANGVRAAPIWDSKKOSFVGMLTTDFILVLHRYYRSPLVQAYEIRGHKIETWREIY
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22. .1500
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22. .1500
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                GGGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTC
                                                                  GGGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTC 139
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AGGGGGAAGGTCCCCGGTCCAGGCCAACTGCTGAGTCCACC
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AX099776
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patent: WO 0120003-A 322-MAR-2001;
INSTITUT MATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
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Rogel-Gaillard,C., Iannuccelli,N., Gellin,J.,
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VGLYSRFDVIHLAAQQTYNHLDMSVGEALRKRTLCLEGVLSCQPHESLGEVIDRIARE
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a 674 c 617 g 498 t
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621 c 560 g 470 t
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 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2115) Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P. A mutation in PKKAG3 associated with excess glycogen content in pice.
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Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
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AVVLETAPILTALDIFYDRRYSALPVYNECGQVVGLYSRFDVIHLAAQOTYNHLDMSV
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EPPGQGEGPRSRPTAESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAG
SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
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Patent WO0120003
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Pred. No. 4.1e-16;
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J., le
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                                                                                                                                                                                                 Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedis University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                        2 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                      skeletal muscle
Science 288 (5469), 1248-1251 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                             l (bases 1 to 1873)
Nilan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Tannuccelli, N., Rask, L., Ronne, H., Rogel-Gaillard, C., Paul, S., Tannuccelli, N., Rask, L., Ronne, H.,
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AF214520.1
                                                                                                                                                                                                                                                                                                                                                                                                                     and Andersson,
                                                                                                                                                                                                                                                                                                                                                                                               A mutation in PRKAG3 associated with excess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF214520 1873 bp mRNA linear MAM 03-JUN Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
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/gene="PRKAG3"
                                                                                                                    /organism-"Sus scrofa"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation "MHFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAP LMDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVS ISPNDSLFEAVYALIKNRIHRLFVLDPVSGAVLHILTHKRLKELHIEGTLLRRSFLYRTIODLGIGTFRDLAVVLETAPLITALDIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNVGEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDE TQHLLGVVSLSDILQALVLSPAGIDALGA"

583 c 529 g 375 t
                               /gene="PRKAG3"
                                                                                                       /chromosome="15"
                                                                                                                                                                       Location/Qualifiers
                                                   tissue_type="skeletal muscle"
. . .1873
                                                                                      /map-"15q"
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/db_xref="taxon:9823"
472. .1389
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/db_xref="GI:13538809"
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Pred. No. 4.6e-09;
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Sus.
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61 agggggaaggtccccggtccaggccagctgctgagtccacc 101
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Sus scrofa
Eukaryota;
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1 (bases 1 to 1873)
Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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Sequence
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Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variants of the gamma chain of ampk, dna sequences encoding
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                                                                                                                          /Protein_id="CAC35800.1"
//Dotein_id="CAC35800.1"
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/db_xref="Gl:815684"
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HFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKOSFVGMLTI
TDFILVLHRYYBSPLVQIYEIEEHKIETWREITLOGGKRFLVSTSPNNDSLEEAVYALI
TDFILVLHRYYBSPLVQIYEIEEHKIETWREITLOGGKRFLVSTSPNNDSLEEAVYALI
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/db_xref="taxon:9823"
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1. .1873
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AVYLETAPILTALDIFVDRRYSALPYVNETGQYYGLYSRFDYIHLAAQQTYNHLDMNY
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82.2%;
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Pred. No. 4.6e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.5%;
al Similarity 82.2%;
83; Conservation
                                                      Andersson,L., Luthman,H. and Marklund,S.
Variants of the human amp-activated protein kinase gamma
Patent: WO 0177305-A 2 18-OCT-2001;
                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                          989 bp
Sequence 2 from Patent WO0177305
AX281579
                                                                                                                                                                                                                                                                                                                                                                                                                                     83;
                                                                                                                                                 Homo sapiens
                                              Arexis AB (SE)
                                                                                                                                                                                              AX281579.1
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INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christlan (DE); Kalm, Ernst (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chardon, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31 from Patent Ax099804
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
∕organism≔"Homo sapiens"
                             Location/Qualifiers
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/db_xrefe"taxon:9823"
623 c 593 g
                                                                                                                Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae,
                                                                                                                                                                                            GI:16608830
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Pred. No. 4.5e-09;
0; Mismatches 18;
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Pred. No. 4.6e-09;
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WO0120003.
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|||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Garand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., WcGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., WcGurk, A., McKernan, K., McPheeters, R., Murphy, T., Naylor, J., Norman, C.H., O'Connort, T., O'Donnell, P., Murphy, T., Naylor, J., Norman, C.H., O'Connort, T., O'Donnell, P., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Santos, R., Schauer, S., Severy, P., Spencer, B., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Submitted (30, MARR-2000) whitchead total total coly, M.
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                                                                                                                                                                                                                                                                                              Submitted (30-MAR-2000) whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, Ma 02141, USA ON Jun 7, 2000 this sequence version replaced g1:7342115. All repeats were identified using RepeatMasker: Smit, A.F.A. 6 Green, P. (1996-1997)
                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-504G11
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Homo sapiens clone RP11-504G11,
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  Center clone name: 504_G_11
Summary Statistics
Sequencing vector: M13; M7781
                                                                                 Center project name:
                                                                                                                   Contact: sequence_submissions@genome
                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center Center code: WIBR
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NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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be preserved.
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Consensus quality: 135376 bases at least 040
Consensus quality: 143264 bases at least 030
Consensus quality: 143263 bases at least 020
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46466 51285: contig of 4820 b
51286 51385: gap of
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1006 1105: gap of 100 bp
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...: gap of
6161: cr
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3 85122: gap of 10
3 93314: contig of 8
5 93414: gap of 10
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42366: contig of 4087 k
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9983: contig of 2336 bp in length
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419: gap of 100 bp
27059: contig of 2640 bp in length
159: gap of 100 bp
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10170: contig of 3011 bp in length
270: gap of 100 bp
33968: contig of 3698 bp in length
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55871: contig of 4486 bp in
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73319. .77115
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85123. .93314
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                                                                                    Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Nov 8, 2001 this sequence version replaced gi:13431203.
                                                                                                                                                                                                                                                                                                                                                                                  MO 63108,
                                                                                                                                                                                                                  Waterston,R.H.
Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Direct Submission
Submitted (08-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001
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The sequence of Homo sapiens
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Sulston, J.E. and Waterston, R.
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Center project name: H_NH0459119
                               Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                              Center: Washington University Genome Sequencing Center Center code: WUGSC
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence restriction digest. more than one subclone; and the assembly was confirmed by

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. I MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc t D.

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) pBACe3.6

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this sequence position l of RP11-459119; actual end is at base position 206854 of RP11-459119. NEIGHBORING SEQUENCE INFORMATION: clone

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 AC009974. A single plasmid region exists between 38812-38903. unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing. ş

FEATURES misc_feature source /note="match 220. .221 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="2" /note="match to /note="similar to Homo sapiens (NID:q14565249)" /clone="RP11-459119" /clone_lib="RPC1-11" /note="match to /note="match to /note="match to EST /note="match to EST BG477625 /note="match to /note="match to /note="match to /note="match to note="match to NID: 914565249 /note="match to EST BI059713 (NID:g14467240)" note="match to EST BE314060 (NID:g9134719)" . 206854 ç EST EST EST BE047599 (NID: g8364652) tz39c01.y1" EST AI670836 (NID:g4850567) wa04g10.x1* EST EST BF304755 EST AL567345 EST BF183086 BG470047 C05773 (NID:g1502549)* BE908408 BE047599 AW880850 (NID: 913402322) (NID: g10402954)" (NID:g8364652) tz39c01.y1* (NID:g13409904)" (NID:g11251653)" (NID: 98042860)" (NID: 912920610) (NID: g11061273)" EST BI114348

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap

between neighboring data submissions

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Best Local Similarity 100. Matches 71; Conservative
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Chemistry: Dye-primer ET; 98% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: phrap; version 0.990319
Consensus quality: 187795 bases at least Q40
Consensus quality: 190513 bases at least Q30
Consensus quality: 192099 bases at least Q20
Insert size: 200000; agarose-fp
Insert size: 194954; sum-of-contigs
Quality coverage: 5.58 in Q20 bases; sum-of-contigs
Quality coverage: 5.57 in Q20 bases; sum-of-contigs
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Submitted (08-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Feb 21, 2001 this sequence version replaced gi:8469048.
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Center code: WUGSC
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Homo sapiens chromosome 2 clone RP11-64705, WORKING DRAFT SEQUENCE,
17 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; 98%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 196554) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACO73128.3 GI:13027579
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jnpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                              as soon as it is available and the accession number be preserved.
                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 196554)
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1257: gap of
3600: contig
3700: gap of
5103: contig
5203: gap of
7: contig of 1157 bp in length
7: gap of unknown length
0: contig of 2343 bp in length
0: gap of unknown length
3: contig of 1403 bp in length
3: contig of 1403 bp in length
4: contig of 3321 bp in length
4: gap of unknown length
4: gap of unknown length
5: contig of 3232 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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130426. .149287
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73917. .92140
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8625. .11856
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113438. .130325
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5204. .8524
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92241. .113337
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11957. .15783
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/db_xref-"taxon:9606"
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of 16888 bp in
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of 13533 bp in
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Query Match

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Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 5888)
Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A.,
Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K.,
Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, University of Agricultural Sciences, BMC Box 597, Uppsala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Andersson,L.
A mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 5888)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., The Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ron LundStrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L.,
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Science 288 (5469), 1248-1251 (2000)
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2771. .2825,3027. .3153,3286. .3451,4578. .4615,4791. .4937,
5294. .5410)
                                                              ALVLSPAGIDALGA"
                                                                       GEALRQRTLCLEGYLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
                                                                                                                                                                                                                                                                                                                                   /product="AMPK gamma subunit"
/protein_id="AAF73989.1"
/db_xref="GI:8215686"
                                                                                                                                                                                                                                                                                                                                                                                                                               /gene-"PRKAG3"
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2771. .2825,3027. .3153,3286. .3451,4578. .4615,4791. .4937,
5294. .>5410)
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/db_xref="taxon:9823"
/chromosome="15"
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                      1638 g
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                      1339 t
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  (PRKAG3) gene, complete cds.
                      3 others
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Sus.
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                           61 agggggaaggt 71
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                                                        TGGGAGAAGGT 8780
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55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular Blotechnology, Beutenberstr. 11, Jena 07745, Germany
NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N. but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
                                                                                                                            h 41.8%; Score 42.2; DB 2;
Similarity 74.6%; Pred. No. 0.1;
53; Conservative 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rump, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF336381 227724 bp DNA linear HTG 02-APR-2001 Mus musculus chromosome 1 clone PAC510; PAC457, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rump,A., Hayes,C., Brown,S.D.M. and Rosenthal,A. Mouse chromosome 1 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus losses 1 to 227724)
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HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse
                                                                                                                                                                                                                                 1. .227724

/organism-"Mus musculus"

/db_xref="taxon:10090"

/chromosome="1"

/clone="PAC510; PAC457"

57663 a 55423 c 56238 g 58199 t
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32747
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77.5%;
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Pred. No. 0.032;
0; Mismatches 16; Indels
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                                                                                                                                                               Length 227724;
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Search completed: October 3, 2002, 14:49:24 Job time: 12084 sec

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                           N_Geneseq_032802:*
1: /SIDS1/gcgdata/g;
2: /SIDS1/gcgdata/g;
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                                                                                                                                   | SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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240.868 Million cell updates/sec
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SUMMARIES	
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31.5 8670 22	31.5 8670 20	71.5 2022 22	4 72.2 71.5 1867 22 AAD03295 5 72.2 71.5 1873 22 AAD03319	98.4 2115 22	98.4 2109 22	100.0	Score Match L	Result Query	ď
X16619 CDNA Clone.	PRKAG3 intron 2 -	Sus scrofa PRKAG3	Pig AMPK gamma sub	Human AMPK gamma s	Human AMPK gamma s	PRKAG3 CDNA Homo	Description		

ALIGNMENTS

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RESULT
AAH43685
                                                                                                         Key
                                                                                                                                          Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                           variation
                                                        variation
                                                                                   variation
                                                                                                                                                                  PRKAG3 cDNA
                                                                                                                                                                               21-JAN-2002
                                                                                                                                                                                              AAH43685;
                                                                                                                                                                                                            AAH43685 standard; cDNA; 1647 BP.
                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                         —
                                                                                                                                                                              (first entry)
                                                        /note=
559
                                                                                   /product= "PRKAG3"
230
                            /note-
1037
            /*tag= d
/label= "C1037T"
                               /*tag- c
/label- "T559C"
/note- "Silent variation"
                                                                                                        Location/Qualifiers 20..1489
                                                                      /label=
                                                                            /*tag= b
    "Causes R340W"
                                                             "Causes P71A"
                                                                    "C230G"
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RESULT
AAD03296
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.
                                                                                                                                                                Human AMPK gamma
                                                                                                                                                                                            13-JUN-2001 (first entry)
                                                                                                                                                                                                                                                      AAD03296 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and refor determining a risk estimate of diseases in subject by detecting
                                                                  Homo sapiens
                                                                                             cystathione beta
                                                                                                            genetic testing;
                                                                                                                           PRKAG3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1647 BP; 346 A; 502 C; 462 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-APR-2000; 2000US-195665P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andersson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AREX-) AREXIS AB
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                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                   61 agggggaaggtccccggtccaggccagctgctgagtccacc 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                              gggccaaagccttgagatggacaaggcagaagtcggtggaggaagggagccaccaggtc 239
                                                                                                                                 gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                      diabetes; obesity; myopathy; cardiovascular disease; anorec testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                         Location/Qualifiers
1..471
          /*tag=
                                                                                             synthase;
                                                                                                                                                                subunit muscle-specific isoform,
                                                                                                                                                                                                                                                      DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                      2109
                                                                                             CBS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 101; DB 22;
Pred. No. 1.3e-20;
Pred. No. 1.3e-20;
                                                                                          cardiant; gene therapy;
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                   AAD03320
                                  RESULT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in PrKag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
AAD03320 standard; cDNA; 2115 BP
                                                                                                                                                                                                                                                                                                                    in a of PF
                                                                                                                                                                                                                                                                                                                             useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
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(ANDE/)
(LOOF/)
                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andersson
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Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-SEP-1999;
18-MAY-2000;
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                                                                        140 agggggaaggtccccggtccaggccaactgctgagtccacc
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                                                                                          61 agggggaaggtccccggtccaggccagctgctgagtccacc 101
                                                                                                                                           08
                                                                                                                                                       1 gggccaaagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence is a cDNA encoding human adenosine monophosphate
                                                                                                                                      gggccaaagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtc 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-244810/25.
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ANDERSSON
LOOFT C.
                                                                                                                                                                                                                                                                                       2109
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                                                                                                                                                                                                                                                                                     ВP;
                                                                                                                                                                                                                                                                                                                is useful in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gellin
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/product= "Human Prkag3 protein"
1390..2109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71pp; English
                                                                                                                                                                                                                                                                                    458 A; 621 C; 560 G; 470 T; 0 other;
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                                                                                                                                                                                                                       98.4%;
99.0%;
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J, Le Roy P, Chardon
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                                                                                                                                                                                                     Score 99.4; DB 22
Pred. No. 4.1e-20;
0; Mismatches 1
                                                                                                                                                                                                                                    DB 22;
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                                                                                                                                                                                                                                    Length
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cc as diabetes, obesity, and disorders associated with muscle metabolism of control of the contr
    Query Match
Best Local Similarity
Matches 100; Conserv
                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorec genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 65-68;
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18-MAY-2000;
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                                                                                                                                               a sequence
PRKAG3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence is a cDNA encoding human adenosine monophosphate
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DB; AAE00223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      as therapeutic for treating carbohydrate metabolism disorders such
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ANDERSSON
LOOFT C.
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2000EP-0401388
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Gellin
                                                                                                     BP;
                                                                                                                                           encoding the is useful in
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1..1395
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                      98.4%;
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                    Score 99.4; DB 22
Pred. No. 4.1e-20;
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    Mismatches
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y P, C
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Chardon P;
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and
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The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                       New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                             Andersson L, l
Iannuccelli N,
                                                                                                                                         Claim 12;
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(ANDE/)
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18-MAY-2000; 2000EP-0401388
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                                                                                                                                                                                                                                                                                                  (KALM/)
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3; diabetes; obesity; myopathy; cardiovascular disease; (
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                                                                                                                                      2; 71pp;
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/product= '
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472..1389
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don P;
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Best Local :
New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plig: gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorec genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                              WPI; 2001-244810/25, P-PSDB; AAE00222.
                                                                                        Andersson L, I
                                                                                                                                                  (ANDE/) ANDERSSON L. (LOOF/) LOOFT C.
                                                                                                                                                                                                             10-SEP-1999; 99EP-0402236
18-MAY-2000; 2000EP-0401388
                                                                                                                                                                                                                                                         11-SEP-2000; 2000WO-EP09896
                                                                                                                                                                                                                                                                                                                  WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preterably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.
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/product= "Sus scrofa complete Prkag3 protein"
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Chardon P;
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4.1e-12;
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The present sequence is a cDNA encoding pig adenosine monophosphate (C) (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, cc complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome CC 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as CC therapeutic for treating carbohydrate metabolism disorders such as CC diabetes, obesity, and disorders associated with muscle metabolism CC such as myopathy and cardiovascular diseases, to modulate AMPK CC activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic CC evaluation, genetic testing and prognosis of a metabolic disorder, CC preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. CC Transgenic animal and host cell transformed with PRKAG3 or heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
   Sequence 1873 BP;
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382 A; 580 C; 535 G; 376 T; 0 other;
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RESULT
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Best Local
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10-SEP-1999;
18-MAY-2000;
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                                                   11-SEP-2000;
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82.2%;
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Pred. No. 4.1e-1
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                                                        Human; AMP-activated protein
metabolic disease; diabetes;
                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
                                                                                                     PRKAG3 intron
                                                                                                                                    21-JAN-2002
                                                                                                                                                                                             AAH43682 standard;
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Matches 71
                                                                                                                                                                                                                (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T a c at nucleotide 1037, resulting in the amino acid substitution of R340W. There may also be nucleotide variation in intron 6.
                                                                                                                                                                                                                                                                                                                  The sequences given in AAH43681-84 represents genomic encoding the human AMP-activated protein kinase gamma (PRKAG3). Detecting the presence of the PRKAG3 DNA, or
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                                                                                                                                        Score 71; DB; Pred. No. 8.4
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AAZ32059

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                                                                                                                                                                                                                                           AAZ32000 and AAZ32001 encode, and AAY49501 and AAY49502 represent, human CC metalloprotease thrombospondin (MEPH) proteins METH1 and METH2 CC respectively. METH1 and METH2 have been found to be potent inhibitors of CC angiogenesis both in vitro and in vivo. They can be used for treating CC cancer and other disorders related to angiogenesis including abnormal CC wound healing, inflammation, rheumatoid arthritis, psorlasis, CC endometrial bleeding disorders, diabetic retinopathy, some forms of CC macula degeneration, haemangiomas, and arterial-venous malformations. CC They may be useful in treating deficiencies or disorders of the immune CC system, by activating or inhibiting the proliferation, differentiation, CC or mobilisation (chemotaxis) of immune cells. The etiology of these CC immune deficiencies or disorders may be genetic, somatic, such as CC cancer or some autoimune disorders, acquired (e.g. by chemotherapy or CC toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and acute conditions. The products can also be used for detection and diagnosis. AAZ32002 to AAZ32080, and AAY49503 to AAY49511 represent sequences given in the exemplification of the present
                                                                                                                          Matches
                                                                                                                                       Query Match
Best Local :
 6522
                                                    6582 GAGGTGGAGGTGGCAGGAGGCGGTGGAGGAGGTGGAGGCAGCGGTATCATGAAACAGCCC 6523
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 431-437; 457pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IRUE/) IRUELA-ARISPE L.
(HAST/) HASTINGS G A.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human: METH1; METH2; anti-angiogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; angiogenesis inhibitor; abnormal wound healing; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lruela-Arispe L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-1998;
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                                                                                                                        Local Similarity es 48; Conserv
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CCCGCCCAACCCCGC
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                                                                                                                                                                                                    8670
                                                                                                                        Conservative
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98US-0098539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             malformation; immune deficiency; ss.
                                                                                                                                                                                                   1624 A;
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                                                                                                                                      31.5%;
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                                                                                                                     Score 31.8; E
pred. No. 3.8;
0; Mismatches
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RESULT

Sequence 8670

BP;

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1359 T; 0 other;

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CANCER
KW CANCER
KW CANCER
KW CANCER
KW CANCER
KW ANGIOL
KW A
                                       The present invention relates to human METH1 and METH2, (ME for metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003).

The present sequence is an expressed sequence tag (EST) for METH. METH can be used for inhibiting anglogenesis in an individual, and for treating cancer, benign tumours, an ocular anglogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, covered to the control control states, and control states, recommendations, hypertrophic scars, nonunion fractures, corponary collaterals, cerebral collaterals, arteriovenous malformations, corponary collaterals, cerebral collaterals, arteriovenous malformations, cischaemic limb angiogenesis, Osler-Webber syndrome, plaque neovascularisation, telangiectasia, haemophillac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH can also be used in birth control. METH can also be used in diagnostic methods for the prognosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METH1 and METH2 polynucleotides and encoded polypeptides, used to inhibit angiogensis in the treatment of disorders such as cancer, rheumatoid arthritis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-AUG-1999;
13-AUG-1999;
22-DEC-1999;
22-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iruela-Arispe L, Hast
Fornwald JA, Terrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IRUE/)
(HAST/)
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JONAK Z L.
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FORNWALD J A.
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SMITHKLINE BEECHAM CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HASTINGS
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99US-0144882.
99US-0147823.
99US-0373658.
99US-0171503.
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC in identifying expressed genes. (I) is useful in gene therapy techniques in victorial control of (II) is useful for generating antibodies against it, detecting or CC in a food supplement. (II) and its binding partners are useful in medical in gene the control of co
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Bost Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 20224; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYSEQ INC.
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  but was obtained in electronic format directly
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Pred. No. 3.
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from WIPO
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CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC is the control of the control o
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Best Local Similarity
Matches 42; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
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23-AUG-2000; 2000US-0649167
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upplement; medical imaging; diagnostic; genetic disorder; ss
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Matches 46
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12-APR-2000; 2000US-196872P.
20-APR-2000; 2000US-199020P.
28-APR-2000; 2000US-200552P.
05-MAY-2000; 2000US-202348P.
11-MAY-2000; 2000US-203495P.
Polypeptides of human transporters diagnosing, treating or preventing
                                                                                   Reddy R, Thornton M,
Gandhi AR, Yao MG,
Policky JL, Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                          Human: transporter and ion channel; TRICH; akinesia; cystic fibrosis; diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia; cardiac disorder; angina; hypertension; myocarditis; hyperglycaemia; neurological disorder; Alzheimer's disease; cataract; infertility; wilson's disease; schizophrenia; Grave's disease; addison's disease; Huntington's disease; multiple sclerosis; meningitis; hypotensive; cardiant; nootropic; neuroprotective; neuroleptic; ophthalmological; nortithered; neuroprotective; neuroleptic; ophthalmological;
                                                                             Walsh
                                                                                                                                        (INCY-)
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                                         2002-017448/02
)B; AAE13285.
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                                                                                                                                       INCYTE GENOMICS INC
                                                                             Lu DAM,
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Hence data for this patent did not appear in the but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "Human transporters
(TRICH)-12"
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA;
                                                                         M, Borowsky ML, T
Sanjanwala MS, E
Seilhamer JJ, Wa
Lu Y, Greene BD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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Pred. No. 13;
0; Mismatches
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and ion channels, useful for disorders of transport,
                                                                    Tang YT, Khan FA, Tribou
Baughn MR, Nguyen DB;
Walia NK, Lal P, Kearney
WD, Raumann BE, Patterson (
                                                                                                                                                                                                                                                                                                                                                                                                                   antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                 and ion channels
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RESULT 13
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ID AAH068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and the polynucleotides encoding them. The composition comprising TRICH CC or agonist of TRICH is useful for treating a disease or condition CRICH is useful for treating a disease or condition CC associated with decreased expression of functional TRICH or condition CC comprising Ab is useful for diagnosing a condition of disease associated with expression of TRICH in a subject, where the disorders include a CC transport disorder such as akinesia, cystic fibrosis, diabetes mellitus, Parkinson's disease, myasthenia gravis, cardiac disorders associated with transport e.g. angina, hypertension, myocarditis, neurological CC disorders associated with transport e.g. Alzheimer's disease, Wilson's disease, schizophrenia, cataracts, inferrility, hyperglycaemia, Grave's CC disease, schizophrenia, cataracts, inferrility, hyperglycaemia, Grave's CC disease, schizophrenia, cataracts, thuntington's disease, dementia, CC multiple sclerosis, bacterial and viral meningitis. TRICH DNA is useful CC for generating a transcript image of a tissue or cell type, which call type and for analysing the proteome of a tissue or cell type. TRICH DNA is used in gene therapy. The present sequence is human call type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                 29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                Ota T, I
Ishii S,
          WPI; 2001-318749/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3901
                                                                        (HELI-) HELIX
                                                                                                                                                                               28-JUL-2000;
                                                                                                                                                                                                       07-FEB-2001.
                                                                                                                                                                                                                                 EP1074617-A2
                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                 Human; primer;
                                                                                                                                                                                                                                                                                                                                     26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                               AAH06841;
                                                                                                                                                                                                                                                                                                                                                                                       AAH06841 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   3961 atcctcctgggaccaggacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4125 BP; 989 A; 1109 C; 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurological, muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 aagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtcaggggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aaggtccccggtccaggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA clone
                                Isogai T,
, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page
                                                                                                 99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                             2000EP-0116126
                                                                        RES
                                                                                                                                                                                                                                                                             detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147-148; 150pp; English
                                                                                                                                                   99JP-0248036
                                                                                                                                                                                                                                                                                                          (5'-primer)
                                Nishikawa
1 T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                       CDNA;
                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to human transporters and ion channels (TRICH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunological and cell proliferative disorders
                                  Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                       886
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3981
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                                                                                                                                                                                                                                                                                                           SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                               Hayashi K,
A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 13;
                                                                                                                                                                                                                                                                                                           NO: 3676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      839
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                               Saito K,
Otsuki
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                                  7
                                           Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                           J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
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ACC XXX ACC XX
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AAH14551/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC of an oligonucleotide comprising a sequence complementary to the Cc complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC clies of sequence, at least 15 nucleotides and the combination of CC the 5'-end sequence is selected from those defined in CC in gene therapy. The primer sets can be used in antisense therapy and CC in gene therapy full-length cDNAs. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the AAH1362B and CC AAH35893 represent human companies and AAH362B to AAH1363C colors of the proteines human amino acid sequences; AAB92446 to CC AAB95893 represent human amino acid sequences; AAB92446 to AAH1363C colors of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                         29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                         07-FEB-2001
   (HELI-) HELIX
                                                                                                                                                                                                                                                                                                                                                      EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA sequence SEQ ID NO:12117
                                                                                                                                                                                                                                   28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH14551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification, where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99CCaaagCCttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtca 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAGAGAAGTCCCCGGGGCCAGCCTGC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 58.051; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                      99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                   2000EP-0116126
RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA; 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    antisense therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy;
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Sequence 1457 BP;

291 A; 442 C;

365

G;

359

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0 other;

present invention

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sequence and an oilgonucleotide comprising a sequence, where the ollgonucleotide which comprises a 3'-end sequence, where the ollgonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH18628 and AAH13633 to AAH18742 represent human cDNA sequences; AB92446 to AAH13639 represent human amino acid sequences; and AAH13629 to AAH13632 represent oilgonucleotides, all of which are used in the exemplification of the property in the primers and property of the primers and AAH13639 to AAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and/or diagnosis of the abnormality of the proteins encoded by full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ishii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; SEQ ID 12117; 2537pp + CD ROM; English
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, Sugiyama
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T, Wakama
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Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a combination
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RESULT 15
AAV59752/c
ID AAV59752 standard; DNA; 1482
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Best Local
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cognitive disorder; schizophrenia; prostate; obesity; osteoclosteoporosis; arthritis; testis; lung; thyroiditis; thyroid; endocrine; metabolism; regulation; malabsorption; gastritis;
                                 Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
                                                                                                                                                                                    Human secreted
                                                                                                                                                                                                                              19-JAN-1999
                                                                                                                                                                                                                                                                   AAV59752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100
                                                                                                                                                                                                                                                                                                                                                                                                        40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ggccaaagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtca 61
                                                                                                                                                                                                                                                                                                                                                                                                    AGAGAGAAGTCCCCGGGGCCAGCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                         gggggaaggtccccggtccaggccagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                protein gene 96 clone HAQBK61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.1%;
58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 29.4;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
neoplasm
                      digestion;
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Ъ δõ В Ş

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11 APR 1997
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07-MAR-1997;
11-APR-1997;
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07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
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11-APR-1997;
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97US-0040162
97US-0040163
97US-0040134
97US-0040334
97US-0040336
97US-0043311
97US-0043313
97US-0043569
97US-0043569
97US-0043576
97US-0043576
97US-0043576
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97US-0047593
97US-0047613
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This sequence represents a nucleic acid molecule designated Gene 96 from the human cDNA clone HADBK61 (deposited as clone ATCC 97897 and ATCC 209043) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human climmunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only.

CC The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV5951) for described uses).
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Kyaw H, L
Ruben SM,
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P-PSDB;
                                                                                                                                                                                                                                                                                                            New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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Lafleur DW, Li Y, Moore PA, I
, Shi Y, Soppet DR, Young PE,
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her CL, Florence KA, Greene JM, Hu JS;
Y, Moore PA, Ni J, Olsen HS, Rosen CA;
DR, Young PE, Yu GL, Zeng Z;
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BG244994 602358260
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BF549656 UI-R-C2-n
BF528844 602070405
BB753946 BB753946
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ALIGNMENTS

JOURNAL MEDLINE COMMENT KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS RESULT 1
AW356079
LOCUS
DEFINITION
ACCESSION
VERSION FEATURES TITLE source Bovidae; Bovinae; Bos.

1 (bases 1 to 399)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA Sequence evaluation of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) BACKWARD: GTTTTCCCAGTCACGACG Plate: 17 row: P column: 9 Seq primer: ATTTAGGTGACACTATAG Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -mins and -minmatch 12 options. Tel: 402 762 4366 Fax: 402 762 4390 USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Contact: Smith TPL 38073 MARC 2BOV Bos taurus AW356079 AW356079.1 GI:6860085 FORWARD: AGGAAACAGCTATGACCAT PCR PRimers Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; /organism="Bos taurus" /db_xref="taxon:9913" Location/Qualifiers 399 bp cDNA 5', mRNA sequence mRNA linear EST 25-APR-2001 -minscore . G.

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Seq primer: ATTTAGGTGACACTATAG
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                                                                                                                                                                                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                       Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka, I. Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizaw, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T. Ishii, Y. and Hayashizaki, Y. Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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                                                                       further details.
                                                                                                                                                                                                                                                                                                                               Konno,H., Fukunishi,Y.,
,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 81-45-503-9216
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                                           e mouse tissues
                                                                                          Please visit our
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse
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RIKEN full-length enriched, 16 days neon
cDNA clone 9630039L22 5', mRNA sequence.
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79.28;
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Rodentia;
                                                                                            site
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Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                          Shibata, K., Itoh, M., Carninci, P., Sugahara
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                                                                                    (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  days neonate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cerebellum
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SOURCE
ORGANISM
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ORIGIN
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JOURNAL
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Best Local
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                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jarel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                          Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001) Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 655)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, C., Sakai, K., Suzuki, H., D., Shibata, K., Shinagawa, A., Shiraki, C., Sakai, K., Suzuki, H., P., Shibata, K., Shinagawa, A., Shiraki, C., Sakai, K., Suzuki, H., P., Shibata, K., Shinagawa, A., Shiraki, C., Sakai, K., Suzuki, H., P., Shibata, K., Shinagawa, A., Shiraki, C., Sakai, K., Suzuki, H., P., Shibata, K., Shinagawa, A., Shiraki, C., Sakai, K., Suzuki, H., P., Shibata, K., Shinagawa, A., Shiraki, C., Sakai, K., Suzuki, H., P., Shibata, K., Shinagawa, A., Shiraki, C., Sakai, K., Suzuki, H., P., Shibata, K., Shinagawa, A., Shiraki, C., Sakai, K., Suzuki, H., P., Shibata, K., Shinagawa, A., Shiraki, C., Sakai, K., Suzuki, H., P., Shibata, K., Shinagawa, A., Shiraki, C., Sakai, K., Suzuki, H., P., Shipagawa, A., Shiraki, C., Sakai, K., Shipagawa, A., Shiraki, C., Sakai, K., Shipagawa, A., Shiraki, C., Sakai, K., Shipagawa, A., Shiraki, C., Shipagawa, Ship
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                           Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB629521 RIKEN full-length enriched, adult male bone cDNA_clone 9830138C07 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tagami, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified pBluescript KS(+) after bulk excision from Lambda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="9630039L22"
/clone_lib="RIKEN full-length enriched, 16 days neonate
cercbellum"
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/lab_host="DH10B"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tagawa, A., Takahashi, F., Takeda, Y.,
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79.2%;
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Pred. No. 2e-07;
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                                                                                                                                         230-0045, Japan
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                                                                                                                                                                                                                                                                                                                      Matches
                                                                                              324 TGGGAGAAGGTGCCCAGTCCAGACCAGCTGCTGAGTCCACC
                                                                                                                                                                                                 264 GAGTCAAGGCTTCCAGATGGACGAGACAGGAGGCCGTAGAGGAAGCAGAACCACCAGGTT 323
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Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.

Func. Genomics 2 pre, L72-L86 (2001)
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e mouse tissues.
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/db_xref="taxon:10090"
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/dev_stage="adult"
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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Unpublished (2001)
Contact war.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 further details
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BB630381
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                                                                               prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-leng cap-trapper. cDNA went through one round of normalizations.
                                                                                                                                                                                                                                                                                                                                       /tissue_type="skin"
/dev_stage="6 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A030014A04"
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                                                                                                                                                                                                                BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: I column: 16
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. vector identified by cross_match with the -minscorv
                                                                                                                                                                                                                                                                                                                                                                                  USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166,
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                          and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, M.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
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467815 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BI775360
BI775360.1 GI:15776346
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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 /note="Vector: pCMV SPORT6; Site_1: xba1; Site_2: xhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

173 c 163 g 93 t
                                                                                         /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                         /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
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5.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Other_ESTs: uk25b05.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 516)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uk25b05.y1 Suc
IMAGE:1970001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:986741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66; Conser
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314 286 1810
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                                                                                       insert. Size selection was performed to exclude fragments <1.5kb</pre> Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCTGCTCTAAAAGCTGCG and 3' end primer
CGACCTGCAGCTGCAGCACA."
                                                                                                                                                                                    /note="Vector: PME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was 119ated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA
                                                                                                                                                                                                                                                                                                                /clone="IMAGE:1970001"
/clone_11b="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL"
/db_xref="taxon:10090"
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Sugano mouse embryo mewa
901 5′, mRNA seguerra
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            Score 53
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Pred. No. 0.00033;
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gctgctgagtccacc 101
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Best Local Similarity
Matches 78; Conserv
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                            cagaagtcggtggaggaaggggagccaccaggtcagggggaaggtccccggtccaggcca 86
TGGGAGAGGGTGCCA-GTCCAGACCAGCTGCTGAGTCCACC 507
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291826 MARC
BF890374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACKWARD: GTTTTCCCAGTCACGACG
Plate: 57 row: H column: 11
Seq primer: ATTTAGGTCACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 444)
Smith, T.P.L. Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 402 762 4366
Fax: 402 762 4390
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                         /tissue_type="pooled"
/lab_host="DHIOB"
/lab_host="DHIOB"
/note="Vector: pcMv SPORT6; Site_1: xbaI; Site_2: xhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
a 147 c 139 g 67 t
                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
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81.3%;
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Pred. No. 0.00099;
0; Mismatches 14;
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                                                                                                                                               Length 444;
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TITLE
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                                                                                                                                                                                                                                         64 gggaaggtccccggtccaggccagctgctg 93
                                                                                                                                                                                                                                                                                                                  4 ccaaagccttgagatggacaaggcagaagtcggtggaggaagggaggccaccaggtcagg 63
                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                     88759831 RIKEN full-length enriched, clone G270121L23 3', mRNA sequence.
Mus musculus
                                                   BB759831.1 GI:16206159
               house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 830.
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Plate: LLAM11495 row: n column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BI754053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5198016"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note "Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                         35.2%;
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Pred. No. 23;
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                                                                                                                                                                                                                                 67 aaggtccccggtccaggccagctgctgagtccacc 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                      AAGCCCTGAGTTCCCCAAGCAGAAGGCAGGGGGGGGAGAAAGGCAGAGGCCAGAGTGGGAGG 198
                                                                                                                                                                                                                                                                                                                                         aagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtcaggggg 66
                                     BB780864
BB780864
              musculus
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RRL:http://genome.gsc.riken.go.jp,

Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura, S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues.
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, W., Hiramoto, K., Hiracka, T., Hirozane, T., Imotani, K., Ishii,
Y. Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Saito, R., Sakai, C., Sakai, T., Sogabe, Y., Suzuki, H., Tagawa
, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 58.9
56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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Contact: Yoshihide Hayashizaki
Caboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,,Y. and Hayashizaki,Y.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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457 bp mRNA RIKEN full-length enriched, col cDNA clone G430068010 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RIKEN full-length enriched, melanocyte"
/cell_type="melanocyte"
130 c 98 g 101 t
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/clone="G270121L23"
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/strain="C57BL/6J"
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Pred. No. 1.1e+02;
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d, colon RCB-0549
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253 AAGGGACCCCGAGCAGGTCTGCTATCAAGTTCAGC 219
                                                                                                   313 AAGCCCTGAGTTCCCCAAGCAGAACGCAGGAGGGAGAAAGGCAGAGGCCACAGTGGGAGG 254
                                                                67
                                                                                                                                            7 aagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtcaggggg 66
                                                    aaggtccccggtccaggccagctgctgagtccacc 101
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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BB780864.1 GI:16941564
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/clone="643068010"
/clone_lib="RIKEN full-length enriched, colon RCB-0549
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/cell_line="RCB-0549 Cle-H3"
145 c 106 g 113 t
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Best Local
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                                                                                                                                                                                                                                                                                                           113 GGCTAAGGACTCCGTAGGGGGCAGGCGGGCAACGGCGGAGCGCTCGGAGCGACCAGGGCC 54
                                                                                                                                                                                                                                                         62 gggggaaggtccccggtccaggccagc 88
                                                                                                                                                                                                                                    53 AGAGAGAAGTCCCCGGGGCCAGCCTGC
                                                                                                                                                                                                                                                                                                                                     2 ggccaaagccttgagatggacaaggcagaagtcggtggaggaaggggggcaccagggtca 61
                                                  BG244994
BG244994.1 GI:12754809
                                                                                      mRNA sequence.
                                                                                                       BG244994 151 bp mrNA linear EST 13-FEB-2001 602358260F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:4486719 5',
                                                                                                                                                                                                                                                                                                                                                                                              l Similarity 60.9
53; Conservative
                house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLANI1465 row: h column: 16
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Tissue Procurement: Life Technologies,
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1 (bases 1 to 736)
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BI765906.1 GI:15757484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:5186367"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                 32.3%;
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                                                                                                                                                                                                                                                                                                                                                                                            Score 32.6; DB 10
Pred. No. 1.2e+02;
0; Mismatches 34
                                                                                                                                                                                                                                      27
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Mus musculus

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KEYWORDS
SOURCE
ORGANISM
         COMMENT
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BB860266
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Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gagatggacaaggcagaagtcggtggaggaagggggggccaccaggtcagggggaaggtcc 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGGTC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGTGGACTCGGCAGACGCCGGTGGAGGGTGAGGATCACCCGGGAAGGGGGGGACGACG 125
                                                                        Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii,
Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Tagawa,
A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
    Unpublished (2001)
Contact: Yoshihide
                                                                 RIKEN Encyclopedia
                                                                                                                                                                                                                                                                                                                                                                                                                              BB860266 RIKEN full-length enriched, pooled cDNA clone G430012004 5', mRNA sequence. BB860266
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                      EST
                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                              house mouse
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Location/Qualifiers
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10330 row: h column: 16
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Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 151)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian
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Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae;
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Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" 38 c 70 g 22 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib~"NCI_CGAP_Mam1"
/tissue_type~"tumor, biopsy sample"
/dev_stage="10 months, virgin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref-"taxon:10090"
/clone="IMAGE:4486719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="FVB/N"
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68.2%;
                                                          of Mouse Full-length cDNAs (Akimura, T., et al.
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Pred. No. 97;
0; Mismatches
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Best Local
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                                                                                                                                                                                                                                                                                                                                            357 ACACCATAGAGAATGTCAAGGCAAAGATCAGGACAAGGAGGGGATCCCCCCTGACCAGCA 416
                                                                                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                                                                                                                                                                 gaaggtccccggtccaggccagctgctg 93
BF549656 479 bp mRNA linear U1-R-C2-ng-f-01-0-UI.rl UI-R-C2 Rattus norvegicus UI-R-C2-ng-f-01-0-UI 5′, mRNA sequence.
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wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib=RKKEN full-length enriched, pooled cell lines*
/note="pooled cell lines; (cell_line=RCB-1754 WEHI 164),
(cell_line=RCB-0264 Meth-17), (cell_line=RCB-035 WEHI-3),
(cell_line=RCB-0569 Weth-18), (cell_line=RCB-0545 OHTA),
(cell_line=RCB-0559 K-1 F1), (cell_line=RCB-1283 B16
melanoma), (cell_type=B cells, cell_line=CRL-1702 WEHI 231
), (cell_type=Leydig cells, cell_line=CRL-2056 MLTC-1),
(cell_type=Mullipotent stem cell, cell_line=CRL-2070 NE),
(tissue_type=bladder, cell_line=RCB-0544 MBT-2),
(tissue_type=bone marrow, cell_type=stroma cell,
cell_line=CRL-2028 SR-4987), (tissue_type=colon,
cell_line=CRL-9049 Cle-H3), (tissue_type=kidney,
cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell_type=B cells, cell_line=CRL-1669 BCL1 Clone 13.20-3B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ), (strain=C3H, tissue_type=brain, cell_line=CRL-1443
BC3H1)*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="G430012004"
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Pred. No.
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AUTHORS
TITLE
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                                                                                                                                                                                                                            Ouery Match 31.7%;
Best Local Similarity 62.5%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
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108 AGAGCCCTGGCCAAGGCAGC
                                                    69 ggtccccggtccaggccagc 88
                                                                                                 48 GACTTGGGCTGCACAAGGCACCAGAGCGTGCAGACTGAGGATGGCCCAGGTGGGGTGGCC 107
                                                                                                                                      9 gccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtcagggggaa 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Soarcs, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoarcs@blue.weeg.uiowa.edu
CDNA Library Preparation: M.B. Soarcs Lab Clone distribution:
Clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID- 1776352
Seq primer: MI3 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       discovery
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                                                                                                                                                                                                                                                                                                                                                                                        //ab_host="blub" (Life Technologies)"
//ab_host="blub" (Life Technologies)"
//ab_host="blub" (Life Technologies) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; The UI-R-C2 library is a subtracted library derived from the UI-R-C3 library; which is a subtracted library derived from the UI-R-C3 library. The UI-R-C3 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present identification of the library of origin of a clone within constructed as follows: PCR amplified CDNA inserts from UI-R-C1 clones from which 3; ESTS had been derived was UI-R-C1 clones from which 3; ESTS had been derived was UI-R-C1 clones from which 3; ESTS had been derived was used as a driver in a hybridization with the UI-R-C1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)"

103 a 163 c 146 g 65 t 2 others
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/strain-"Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="UI-R-C2-ng-f-01-0-UI"
/clone_lib="UI-R-C2"
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127
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Pred. No. 1.6e+02;
0; Mismatches 30; Indels
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Search completed: October 3, 2002, 16:15:04 Job time: 16959 sec

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Minimum DB
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Listing first 45 summaries
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                             seq length: 0 seq length: 2000000000
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1: /cgn2_6/ptcodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptcodata/2/ina/6A_COMB.seq:*
3: /cgn2_6/ptcodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptcodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptcodata/2/ina/backfiles1.sec
6: /cgn2_6/ptcodata/2/ina/backfiles1.sec
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                       383533 seqs, 122816752 residues
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Gapop 10.0 , Gapext 1.0
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101
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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               US-09-404-650-12
US-08-76-859-1
US-08-776-859-1
US-08-776-859-1
US-08-826-532-1
US-08-826-532-1
US-09-128-324A-1
US-09-138-922-3
US-08-105-989-3
US-08-105-989-3
US-08-164-9238-15
US-08-164-2928-17
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US-08-845-623-17
US-08-845-623-27
US-08-815-927-15
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Sequence 1, A
Sequence 1, A
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Sequence 1, B
Sequence 1, B
Sequence 3, B
Sequence 10,
Sequence 7, B
Sequence 11, B
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                  Sequence
       appli e 1, Appli e 3, Appli e 3, Appli e 10, Appli e 17, App
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US-08-800-840-1
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; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-404-650-12
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                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08800840 Patent No. 6060288
                                                       GENERAL INFORMATION:

APPLICANT: Adams, Christopher P.

APPLICANT: Beles, Truett C.

APPLICANT: Muir, Andrew R.

APPLICANT: Kron, Stephen J.

TITLE OF INVENTION: Method and Apparatus for Performing
TITLE OF INVENTION: Amplification of Nucleic Acis on Supports
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESS:

ADDRESS:

Control of Nucleic Acis on Supports
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
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STREET: Two Mil CITY: Lexington
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                                               ADDRESSEE: Hamilton, Brook,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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24.8	24.8	25.0	25.1	25.1	25.3	25.3	25.9	26.5	26.5	26.5	26.5	26.5	26.5	26.5	26.5	26.5	26.5
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PCT-US95-02689-51	US-08-207-481-44	US-08-343-443B-97	5449756-1	5198359-1	US-09-103-840A-1	US-09-103-840A-2	US-09-328-111-464	US-09-103-330-35	US-09-103-330-25	US-09-103-330-23	US-09-103-330-21	US-09-103-330-19	US-09-103-330-17	US-09-103-330-15	US-08-815-927-25	US-08-815-927-23	US-08-815-927-21
Sequence 51, Appl	٠,	Sequence 97, Appl		Patent No. 5198359	Sequence 1. Appli		464	ω <u>.</u>	25	23	21	9	17	15	25	Sequence 23, Appl	Sequence 21. Appl

ALIGNMENTS

Sequence 12, Application US/09404650 Patent No. 630988 GENERAL INFORMATION: APPLICANT: Dietrich, Paul S. APPLICANT: McGivern, Joseph G. TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF; TITLE OF INVENTION: AND USES FILE REFERENCE: R0043B-REG sequence listing CURRENT APPLICATION NUMBER: US/09/404,650 CURRENT EPLICATION NUMBER: US/09/404,650 NUMBER OF SEQ ID NOS: 12 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 12

28.5%;

Score 28.8; DB Pred. No. 4.1; 0; Mismatches

BB 32; 4.

Length 6503; Indels

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Gaps

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Smith & Reynolds, P.C.

STATE: Massachusetts

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US-08-800-840-1
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                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08776859
Patent No. 6090592
LENGTH: 268
TYPE: DNA
ORGANISM: Homo sapiens
-08-776-859-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                      APPLICANT: Mosaic Technologies, Inc.
APPLICANT: Adams, Christopher P.
APPLICANT: Kron, Stephen J.
TITLE OF INVENTION: Method and Apparatus for
TITLE OF INVENTION: Amplification of Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                             NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                       EARLIER APPLICATION NUMBER: 08/285,385 EARLIER FILING DATE: 1994-03-08
                                                                                                                                                     FILE REFERENCE: MOSAIC
CURRENT APPLICATION NUMBER: US/08/776,859
CURRENT FILING DATE: 1997-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MST9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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LENGTH: 268 base pairs
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APPLICATION NUMBER: PCT/US95/09905
FILING DATE: 03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION UNDER: US 08/285,385
PILLING DATE: 03-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,840
FILING DATE: 14-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                            110 TGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                               61 agggggaaggtcccccggtccaggccagctgctgagtcca 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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N: 435
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Pred. No. 2.6;
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Acids on Supports
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                                                        Matches
                                                                         Query Match
Best Local
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GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                   TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA MOLECULE TYPE: NO
                                                                                                                                                        HYPOTHETICAL: N
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: B0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/285,385 FILING DATE: 03-AUGUST-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US99
FILING DATE: FILED HEREWITH
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 tgggcataaaagtcagggcagagccatctattgcttaca 148
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                    NAME: JANIUK, ANTHONY
                                                                       Local
                                                                                                                                                                                                                                                        LENGTH:
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                                                       l Similarity 55.6
55; Conservative
                                                                                                                                                                                                                                         nucleic acid
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55; Conservative
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                                                                                                                                                                                                                                                     268 base pairs
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                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                linear
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                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                             double
                                                                    28.3%;
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55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHOD AND APPARATUS FOR PERFORMING AMPLIFICATION OF NUCLEIC ACIDS ON SUPPORTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT/US95/09905
                                                     Score 28.6; DB Pred. No. 2.6; 0; Mismatches
                                                        0;
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Pred. No. 2.6;
0; Mismatches
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                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-228-324A-1
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, TYPE: DNA
; ORGANISM: Homo sapions
US-08-826-532-1
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                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 428
                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09228324A Patent No. 6335184
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Hest Local Similarity 55.6
Matches 55; Conservative
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TITLE OF INVENTION: Linked Linear Amplification of Nucleic Acids
FILE REFERENCE: 3239-1029
CURRENT APPLICATION NUMBER: US/08/826,532B
CURRENT FILING DATE: 1997-04-02
EARLIER APPLICATION NUMBER: US 08/475,605
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatenLIN Ver. 2.0
SEQ ID NO 1
                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 08/826,532 PRIOR FILING DATE: 1997-04-02 NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/228,324A CURRENT FILING DATE: 1999-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reyes, Antonio A
APPLICANT: Wallace, Robert B.
APPLICANT: Ugozzoli, Luis A.
APPLICANT: Ugozzoli, Luis A.
TITLE OF INVENTION: Linked Linear Amplification of Nucleic Acids
     73
                  61 agggggaaggtccccggtccaggccagctgctgagtcca 99
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                                                                               73 tgggcataaaagtcagggcagagccatctattgcttaca 111
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                                                            tgggcataaaagtcagggcagagccatctattgcttaca 111
                                                                                                                                        Conservative
                                                                                                                                                      28.3%;
55.6%;
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                                                                                                                                    Score 28.6; DB 4; Length 428; Pred. No. 2.8; 0; Mismatches 44; Indels
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Pred. No. 2.8;
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US-08-105-989-3
                                                                                                                                             Sequence 3, Application US/09138922 Patent No. 6147202
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                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
CCOUNTRY: U.S.A.
ZIP: 10036-Z711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                            APPLICANT: Kumar, Ramesh
APPLICANT: Sharma, Ajay
APPLICANT: Paulhiao, Clara
APPLICANT: Khoury-Christianson, Anastasia P.
APPLICANT: Midha, Sunita
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 596 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OB/105,989
FILING DATE: 11-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: COPUZZÍ, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 679
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                    491 TGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACA 529
                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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APPLICANT: Sharma, Ajay
APPLICANT: Paulhiac, Clara
APPLICANT: Khoury-Christianson, Anastasia
APPLICANT: Midha, Sunita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Production of Human Hemoglobin in TITLE OF INVENTION: Transgenic Pigs.
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                                                                                                                                                                                                                                                                                  61 agggggaaggtccccggtccaggccagctgctgagtcca 99
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STATE: New York
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55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : (212) 790-9090
(212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Production of Human Hemoglobin in Transgenic Pigs.
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Pred. No. 3;
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                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 44;
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

ADDRESSEE: STREET: 1

1155 Avenue of the Americas

PENNIE & EDMONDS

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US-08-550-715-10 : Sequence 10, A
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Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/105,989
FILING DATE: 11-AUG-193
ATTORNEY/AGENT INFORMATION:
NAME: COCUZZI, LAUGA A.
REGISTRATION NUMBER: 30,742
REFERENCE/JOCKET NUMBER: 6794-030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1070-064-0771
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
     COMPUTER READABLE FORM:
MEDIUM TYPE: F1Dpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                         tent No.
                                                                                                                                                                                                                            TITLE OF INVENTION:
CURRENT APPLICATION DATA:
                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 596 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                491 TGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACA 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                      431
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                                                                                                                           CITY: Chicago
STATE: Illinois
                                                                                               ZIP: 60606-6402
                                                                                                              COUNTRY:
                                                                                                                                                             STREET:
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                                                                                                                                                                           ADDRESSEE:
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STATE: New York
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                                                                                                                                                        6300 Sears Tower,
                                                                                                                                                                                                                                                         Bowle,
                                                                                                          United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                           Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double

    Lemuel J.
    Human `Thalassemia Mutations as a Predictor of
    Blood-Related Disorders

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.3%;
                                                                                                                                                        , O'Toole,
fower, 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28.6;
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                        Gerstein, Murray & South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
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RESULT 10
PCT-US96-09430-7
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; LOCATION:
US-08-550-715-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Applicati
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
TELEFAX: 301-208-6997 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 301-527-2058
                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Glazer, Peter M.
TITLE OF INVENTION: TREATMENT OF HEMOGLOBINOPATHIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Gass, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601 TGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACA 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                         NAME: Karta, Glenn E. REGISTRATION NUMBER:
                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                            TELEPHONE:
                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 agggggaaggtccccggtccaggccagctgctgagtcca 99
                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                           CITY: Gaithersburg
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les 55; Conserv
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TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                            200 Perry Parkway
                                 301-208-6997
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linear
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Pred. No. 3.9;
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US-08-289-653-2/c

: Sequence 2, Application US/08289653

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                                                                         INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1140 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.3%;
Bost Local Similarity 55.6%;
Matches 55; Conservative
             ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/887
FILING DATE: May 22, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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                                                              HYPOTHET ICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2101 TGGGCATAAAAGTCAGGGCCAGAGCCATCTATTGCTTACA 2139
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POSITION IN GENOME:
CHROMOSOME/SEGMENT: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kazuaki KITANO et al.
TITLE OF INVENTION: DNA AND ITS USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
ORGANISM: Fusarium sp.
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 805 Fifte
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatibl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                              Genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inch, 500
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RESULT 12
US-08-289-653-1/c
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; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-289-653-2
                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08289653 Patent No. 5543322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Kazuak
                                         COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
                                                                                                                  ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                        STREET: 805 Fiftee
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                    APPLICANT: Kazuaki KITANO et al.
TITLE OF INVENTION: DNA AND ITS
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 CCTTGAGCTTGACAATGTACTTGCCAGCAATGGGCTGCGAACCACGAGCCTCGAGGAGAG 65
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                               FILING DATE:
                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                         70 gtccccggtccaggccagctgctgag 95
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JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAGES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
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                                                                                                                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                    Diskette, 5.25 inch, 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.5%;
                                            US/08/289,653
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Pred. No. 12;
0; Mismatches
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RESULT 13
US-08-164-292B-15/c
; Sequence 15, Application US/08164292B
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                                                                                                                                                                                                                     Query Match
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ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
NAME: Warren M. Cheek, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2845 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMPUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                     605 GAGCGGGTTCCAGGACCGGGGCCGCG 580
                                                                                                                          665 CCTTGAGCTTGACAATGTACTTGCCAGCAATGGGCTGCGAACCACGAGCCTCGAGGAGAG 606
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ORIGINAL SOURCE:
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                                                                                      70 gtccccggtccaggccagctgctgag 95
                                                                                                                                           10 ccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtcagggggaag 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMEDIATE SOURCE:
                                                                                                                                                                                          Local Similarity es 49; Conserv
                                                                                                                                                                                                                                                                                           FILING DATE:
PUBLICATION DATE:
                                                                                                                                                                                                                                                                                                                      DATE:
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL:
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Pred. No. 14;
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US-08-164-292B-17/c
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FILING DATE: 09-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 29,216
REFERENCE/DOCKET NUMBER: 2931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 677-7000
TELEPAX: (415) 677-7522
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 5100 base pairs
                                                                                                                                                                                        Sequence 17, Application US/08164292B Patent No. 5820868
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.5%;
Best Local Similarity 61.4%;
Matches 43; Conservative
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APPLICANT: MAITTAL, S
APPLICANT: GRAHAM, F
APPLICANT: PREVEC, L
APPLICANT: BABIUK, L
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                    GENERAL INFORMATION:
                                      APPLICANT: MITTAL, SURESH K.
APPLICANT: GRAHAM, FRANK L.
APPLICANT: PREVEC, LUDVIK
APPLICANT: BABIUK, LORNE A.
TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION IN BOVINE
TITLE OF INVENTION: ADEMOVIRUS EXPRESSION VECTOR SYSTEM
                  NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                               1682 GTCTTGAGGAGGACGGGAGGCACTCGGCGTGGGAACAGGAACAGCGGATGCTGCCGGAA 1623
                                                                                                                                                                                                                                                                                                           1622 GCTCCCTGGT 1613
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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    ADDRESSEE:
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LOCATION: 2..418
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TYPE: nucleic acid
STRANDEDNESS: double
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STATE: California
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MORRISON & FOERSTER
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FRANK L.
LUDVIK
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RECOMBINANT PROTEIN PRODUCTION IN BOVINE ADENOVIRUS EXPRESSION VECTOR SYSTEM
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Pred. No. 16;
0; Mismatches
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345 California Street

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RESULT 15
US-08-164-292B-19/c
; Sequence 19, Application US/08164292B
**Arent No. 5820868
**Arent No. 5820868
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: MITTAL, SURESH K.
APPLICANT: GRAHAM, FRANK L.
APPLICANT: PREVEC, LUDVIK
APPLICANT: BABIUK, LORNE A.
TITLE OF INVENTION: RECOMBINANT PROTITLE OF INVENTION: ADENOVIRUS EXPRIBED SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 345 California Street
CTTV. Can FERENCIECO
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Best Local Similarity 61.4%;
Matches 43; Conservative
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AMAE: GRACEY, NANCY J.
REGISTRATION NUMBER: 29,216
REFERENCE/DOCKET NUMBER: 29310
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 677-7000
TELEFAX: (415) 677-7522
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1622 GCTCCCTGGT 1613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
STATE: California
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CITY: San Francisco
STATE: California
                                                                                                                    COUNTRY: USA
ZIP: 94104-2675
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LOCATION: 408..1331
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VENTION: RECOMBINANT PROTEIN PRODUCTION IN BOVINE
VENTION: ADENOVIRUS EXPRESSION VECTOR SYSTEM
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Pred. No. 16;
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ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 29,216
REFERENCE/DOCKET NUMBER: 2931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 677-7900
TELEFAX: (415) 677-7522
TELEFAX: 44-0154
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      Query Match 26.5%;
Best Local Similarity 61.4%;
Matches 43; Conservative
                                                                                                                                                  1682 GTCTTGAGGAGGACGGGGAGGCACTCGGCGTGGGAACAGGAACAGCGGATGCTGCCGGAA 1623
                                                                                 1622 GCTCCCTGGT 1613
                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                       69 ggtccccggt 78
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LOCATION: 529..954
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
        Score
              Query
Match Length DB
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LSPQAEPPKLGWDDELIKRGAGOLYMRRWGEHTCYDAMATSSKLVIFDTMLEIKKAFFA
LSPQAEPPKLGWDDELIKRGAGOLYMREMGEHTCYDAMATSSKLVIFDTMLEIKKAFFA
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LQGCFKPLVSISPNDSLFEAVYTLIKHRIHRLPVLDFVSGNVLHILTHKRLLKFLHIF
GSLLPRPSFLVRTIQDLGIGTFRDLAVYLETAPITALDFVDRRVSALPVVNECGQV
VGLYSREDVIHLAAQQTYNHLDMSVGEALRQRTLCLEEVLSCQPHESLGEVIDRIARE
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 2115)
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy
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INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Sweniversity of Agricultural Sciences, BMC box 597, Uppsala 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 2115)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Mogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                skeletal muscle
Science 288 (5469), 1248-1251 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                             /product="AMP-activated protein kinase gamma subunit"
/protein_id="AAF73987.1"
/db_xref="GI:8215682"
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/note="AMPKG3"
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                                                                            Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Unpublished
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1 (bases 1 to 152129)
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Center: Whitehead Institute/ MIT Center for Genome Research
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SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
RFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTI
TDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAYYTLI
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Pred. No. 1.4e-17;
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                           38180 38279; gap of 100 bp

38280 42366; contig of 4087 bp

42367 42466; gap of 100 bp

42467 46365; contig of 3899 bp

46366 46465; gap of 100 bp

46466 51285; contig of 4820 bp

51286 51385; gap of 100 bp
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Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases;
Quality coverage: 3.3 in Q20 bases;
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Contact: sequence_submissions@genome.wi.mit.edu
Project Information
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1006 1105: gap of 100 bp
1106 2402: contig of 1297 bp in length
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60695: gap of 100 bp
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201: gap of
7547: cc.
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695: gap of 1
73218: contig of
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77216 85022: contig of 7807 bp in length
85023 85122: gap of
85123 9314: contig of 8192 bp in length
93315 93444: gap of
100 bp
93415 101193: contig of 7779 bp in length
101194 101293: gap of
101294 13990: contig of 1797 bp in length
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           * NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                               Sequencing vector: M13; 988
Sequencing vector: plasmid; 08
Chemistry: Dye-primer ET; 988 of reads
Chemistry: Dye-terminator Big Dye; 08 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 187795 bases at least 040
Consensus quality: 190513 bases at least 030
Consensus quality: 19099 bases at least 020
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On Feb 21, 2001 this sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 196554)
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AC073128
AC073128.3 GI:13027579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACO73128

Homo sapiens chromosome 2 clone
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93415. .101193
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/note="assembly_fragment"
85123. .93314
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101294. .113090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001 this sequence version replaced gi:8469048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 101; DB 2 100.0%; Pred. No. 1e-17;
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RP11-64705,
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73917. .92140
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113438. .130325
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5204. .8524
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22007. .28887
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8625. .11856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding Biochem. J. 346 Pt 3, 659-669 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carling, D.
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AMP-activated protein kinase; AMPK gamma 3 gene;
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                /translation="MEPGLEHALRRTPSWSSLGGSEHQEMSFLEQENGSSWPSPAVTS
SSERIRGKRRAKALRWTROKSVEEGEPPGOGEGPRSRPAAESTGLEATFPKTTPLAQA
DPAGVGTPSTGWDCLPSDCTASAAGSSTDDVELATEFPATEARCELEGLLEERPALC
LSPQAPFPKLGWDDELRKPGAQIYMRFIEEHTCYDAWATSSKLVIFDTMLEIKKAFFA
LVANGVRAAPLWDSKKOSFVCMLTITDFILVLHRYYRSPLVOIYEIEQHKIETWREIY
LOGCFKPLVSISPNDSLFEAVYTLIKNRIHTLFVLDBVSGNVLHILTHKKFLHIF
GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQV
VGLYSRFDVIHLAAQOTYNHLDMSVGEALRKRTLCLEGVLSCOPHESIGEVIDRIARE
QVHRLVLVDETQHLLGVVSLSDLQALVKSPAGIDPSGPEKI"
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/product="AMP-activated protein kinase
/protein_id="CaB65117.1"
/db_xref="GI:6688201"
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                                                                                                                                                                                                                                                                                                                  /gene-"AMPK gamma 3"
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/db_xref="taxon:9606"
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                                                                                                                                                                           Direct Submission
Sibmilted (03-VAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 206854)
                                                                                                                                                Direct Submission
                                                                                                                                                               Waterston, R.
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Waterston, R.H.
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Submitted (08-NOV-2001) Genome
University School of Medicine,
MO 63108, USA
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Submitted (08-SEP-1999)
University School of Med
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Sulston, J.E. and Waterston, R.
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Center: Washington University Genome Sequencing Center Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@watson.wustl.edu
Center project name: H_NH0459I19
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              donor, as described by Oscegawa, K. Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An Improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://www.cancer.med.buffale.edu)
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VECTOR: pBACe3.6
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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/clone_lib="RPCI-11"
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/db_xref="taxon:9606"
/chromosome="2"
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Rogel-Gaillard,C., Iannuccelli,N., Gellin,J.,
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Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
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LMDSKKQSFVGMLTITDDFILVLHRYVRSPLVQIYEIEBHKIETWREIYLQGCFKPLVS
ISPNDSLFEAVYALIKNRIHRLEVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFL
XRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVI
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Sutheria; Cetartiodactyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                                                                                                        71.78;
83.78;
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Pred. No. 8.2e-10;
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                                                                                                                    1873 bp mRNA
protein kinase
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                                                                                                                  gamma subunit (PRKAG3)
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J., le
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                                                                                                                                MAM 03-JUN-2000
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Sus.
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Ernst
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AUTHORS
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Best Local S
Matches 82
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AUTHORS
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                                                                                                                                                                                                                                                                                                4 teccegeaggeeceattteceaagetgggetgggatgaegaactgeggaaaceeggegee 63
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                                                                                                                                                                                                                   CAGGTCTACATGCACTTCATGCAGGAGCACACCTGCTA 506
                                      pig.
Sus scrofa
                                                                                                       AX099800
Sequence 27 from Patent
AX099800
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                         AX099800.1
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kalm, E., Le Roy, p. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A mutation in PRKAG3 associated with excess glycogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 288 (5469), 1248-1251 (2000) 20280150
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GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
GSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
HEMQEHTCYDAMATSSKLVIFDTMLEIKAFFALVANGVRAAPLWDSKKQSFYGMLTI
TDFILVLHRYRSPLVQIYEIEBHKIETWREIYLQGCFKPLVSISPNDSLFEAVYALI
TOFILVLHYRYRSPLVQIYEIEBHKIETWEIYLQGCFKPLVSISPNDSLFEAVYALI
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AVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product "AMP-activated protein kinase gamma subunit"
/protein_id="AAF73988.1"
/db_xref="GI:8215684"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="skeletal muscle"
1. .1873
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/db_xref="taxon:9823"
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1. .1873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="PRKAG3"
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                                                                                      GI:13538834
                                                                                                                                                                                                                                                                                                                                                                   71.78;
83.78;
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Pred. No. 8.2e-10;
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              Euteleostomi;
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           Query Match
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGGTCTACATGCACTTCATGCAGGAGCACACCTGCTA 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCCCAGAGGTGCTGTTACCCAGGCTGGGCTGGGATGATGAGCTGCAGAAGCCGGGGGCC
                                                                                                                                         Variants of the gamma chain of ampk, dna same, and uses thereof Patent: WO 0120003-A 31 22-MAR-2001; INSTITUT NATIONAL DE LA RECHERCHE AGRONC Andersson, Leif (SE); Looft, Christian
                                                                                                                                                                                                                                Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Tannuccelli, N., Gellin, J., le Roy
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                     pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                  AX099804 2022 bp
Sequence 31 from Patent WO0120003
AX099804
                                                                                                                                                                                                                             Chardon, P.
                                                                                                                                                                                                                                                                                                                                                                     AX099804.1
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INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
                                                                                                                                                                                                                                                                      (bases 1 to 2022)
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Rogel-Gaillard, C., Iannuccelli, N., Gellin, J.,
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Andersson, L., Looft,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         same, and uses
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                                                                      412
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                                                                 /organism="Sus scrofa"
/db_xref="taxon:9823"
623 c 593 g
                                                                                                                              Location/Qualifiers
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/Protein_id="CaC35800.1"
/Protein_id="CaC35800.1"
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GPGPREGPGSRPVAESTGQEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
DSNTDHLDLGIEFSASAASGDELGLVEEKPAFCPSPEVLLPRLGWDDELQKPCAQVYM
HFWQEHTCYDAWATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTI
TDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKJSPNDSLFEAVYALI
KNRIHRLDVLDPVSGAVLHILTHKKLLKFLHIFGTLLPRPSFLYRTIODIGIGTFRDL
KNRIHRLDVLDPVSGAVLHICHKRYNNETGQVVGLYSRFDVIHLAAQOTYNHILDMNV
GEALRQRTLCLEGVLSCOPHETLGEVIDRIVRBQVHRLVLVDETQHLLGVVSLSDILQ
GEALRQRTLCLEGVLSCOPHETLGEVIDRIVRBQVHRLVLVDETQHLLGVVSLSDILQ
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580 c 535 g
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/db_xref="taxon:9823"
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83.7%;
         71.78;
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Pred. No. 8.2e-10;
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      72.4;
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    6;
    Length 2022;
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J., le Roy,P.
                                                                                                                                                                                                                                   Roy,P.
                                                                                                                                                                                                                                                                                 Euteleostomi;
Sus.
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Matches 82; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and (University of Agricultural Sciences, BMC Box 597,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 5888)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       skeletal muscle
Science 288 (5469),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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/gene="PRKAG3"
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join(1. .154,515.
2771. .2825,3027.
                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                  /gene="PRKAG3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Sus scrofa"
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1. .2825,3027. .3153,3286. .3451,4578.
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AUTHORS
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                                                                                                                                  Ouery Match 71.7%; Score 72.4; DB 2; Length 227724; Best Local Similarity 83.7%; Pred. No. 5.8e-10; Matches 82; Conservative 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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source
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Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus chromosome 1 clone PAC510; PAC457, *** PROGRESS ***, 3 unordered pieces. AF336381 AF336381.1 GI:13507298 HTG; HTG2-PHASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rump,A., Hayes,C., Brown,S.D.M. and Rosenthal,A. Mouse chromosome 1 genomic sequence
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/ 55423 c 56238 g 58199 t
                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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17969: gap of unknown length
32746: contig of 14777 bp in length
32846: gap of unknown length
227724: contig of 194878 bp in length.
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Search completed: October 3, 2002, 14:49:54 Job time: 12114 sec

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                                                  PRKAG3 intron 2 -
PRKAG3 cDNA. Homo
Human AMPK gamma s
Human AMPK gamma sub
Pig AMPK gamma sub
Pig AMPK gamma sub
Sus scrofa PRKAG3
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        DNA encoding
                             Pseudomonas aerugi
RESULT
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ID AAH4
XX AAH4
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524	524	524	524	524	2325	8899	4466	2664	2365	2365	2365	1802	874	1962	876	876		27671		1803	1319	3267	3184	2184	669	2175	14533	7818	7816	3593	3406	1406	5122	4397	3918
22	22	22	22	22	23	22	23	18	21	21	20	22	21	22	22	22	21	21	23	23	23	19	19	19	21	22	23	22	22	23	23	23	23	23	23
AAI40957	AAK35241	AAK09352	ABA28966	ABA61059	AAS54311	ABA21236	ABL02978	AAT38449	AAC58230	AAC78486	AAZ34002	AAH89959	AAD02325	AAK94805	AAK93756	AAK92035	AAF21611	AAA81474	ABL14872	ABL14873	ABL02979	AAV34326	AAV34328	AAV34327	AAF12737	AAL04858	AAS65883	AAK51950	AAK52934		950	o	334	AAS74446	AAS80424
#9643	bone m	brain exp	#7432 for g	Human foetal liver	Pseudomonas aerūgi	Human nervous syst	Drosophila melanog	cDNA for DNA polym		PRO351	PRO351		serin	full-lengt		Human cDNA 5'-end	Neisseria meningit	N. meningitidis pa		Drosophila melanog	Drosophila melanog	Human glycogenin-2	Human glycogenin-2	ָר מים	r	n reproductiv	ncodina	001	Human polynucleoti		æ	sophila me	encoding	encoding	DNA encoding novel

ALIGNMENTS

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Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAH43682 standard; DNA; 989 BP.
                                                                                                                                                                                                                                                                                                                                 PRKAG3 intron 2 - intron 4.
                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                              21-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                           AAH43682;
                                                                                                                                                                                                                                                                                                                                                          (first entry)
                              /number= "Exon 4"
946..989
                                                                        /*tag= c
/number= "Intron
542..945
                                                                                                                  /number=
178..541
                                                                                                                                                             /note= "3'
22..177
/*tag= e
/number= "Intron
                                                          /*tag- d
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                                                                                                                                                                                                                                 Location/Qualifiers
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portion o
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RESULT
AAH4 3685
1D AAH4
XX AAH4
AC AAH4
AC AAH4
XX DT 21-C
XX Huma
KW Huma
KW metac
XX Homc
CX Homc
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340w. There may also be nucleotide variation
              variation
                                                                                      Homo
                                                                                                           metabolic disease;
                                                                                                    Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                                                                                                                                               PRKAG3 cDNA
                                                                                                                                                                     21-JAN-2002
                                                                                                                                                                                              AAH43685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,
                                                                                                                                                                                                                    AAH43685 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 2;
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                                                                                    sapiens
                                                                                                                                                                                                                                                                                         gcccagatctacatgcgcttcatgcaggagcacacctgcta 101
                                                                                                                                                                                                                                                                                                                          ctgtccccgcaggccccatttcccaagctgggctgggatgacgaactgcggaaacccggc 852
                                                                                                                                                                                                                                                                              gcccagatctacatgcgcttcatgcaggagcacacctgcta
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230
                                               Location/Qualifiers 20..1489
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                       "PRKAG3"
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                                                                                                                                                                                                                                                                                                                                                                             Score 101; I
Pred. No. 9.8
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                        101; DB 22;
No. 9.8e-23;
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RESULT
AAD03296
ID AAD0
XX
AC AAD0
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DT 13-J
XX
DE Huma
                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                             This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R71A; in exon 4 variation be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R71A; in the may also be variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.
        Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA
                                       13-JUN-2001
                                                                  AAD03296
                                                                                                                                                                                                                                                                                                                                        Sequence 1647
                                                                                            AAD03296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 5; 25pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and for determining a risk estimate of diseases in subject by detecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-APR-2000; 2000US-195665P
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                                                                                                                                                                                                                                                                       101;
                                                                                                                                                                                                                                                                                    Similarity
                                                                                            standard;
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                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                        BP; 346 A; 502 C;
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559
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1037
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"T559C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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                                                                                                                                                                                                                                                                       0,
                                                                                         ВP
                                                                                                                                                                                                                                                                    Score 101; DB 22;
Pred. No. 1.1e-22;
Mismatches 0;
                                                                                                                                                                                                                                                                  Mismatches
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В Ş Вb

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Matches
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Best Local
                                                                                                                                                   useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of pRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of pRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding pRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of pRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                          evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
                                                                                                                                                                                                                                                                                                                      useful as therapeutic for treating carbohydrate metabolism disorders as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andersson L, |
| Iannuccelli N,
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5'UTR
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18-MAY-2000;
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ctgtccccgcaggccccatttccccaagctgggctgggatgacgaactgcggaaacccggc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-244810/25
                                                 Similarity 100.
01; Conservative
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diabetes; obesity; myopathy; cardiovascular disease; anorecti
testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 2; 71pp; English
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2000EP-0401388
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Gellin
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472..1389
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/product= "
1390..2109
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                                                                                                                             458 A; 621 C;
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                                             J.08;
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J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _"Human Prkag3 protein"
                                                 Score 101; DB Pred. No. 1.1e-; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               opathy; cardiovascular disease; anorec
metabolism disorder; skeletal muscle;
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able to modulate AMPK activity

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CC (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, CC complete PRKAG3. Mutation in Prkag3 results in an altered regulation of CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is CC useful as therapeutic for treating carbohydrate metabolism disorders such CC as diabetes, obesity, and disorders associated with muscle metabolism Such as myopathy and cardiovascular diseases, to modulate AMPK CC activity, and for restoring a normal AMPK function. PRKAG3 sequence CC and its functionally altered mutants are useful for the diagnostic CC evaluation, genetic testing and prognosis of a metabolic disorder, CC preferably a carbohydrate metabolism disorder. Primers that can detect CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are CC useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3 or a functionally altered allele of PRKAG3 or a sequence consisting of PRKAG3 or its mutant, are useful for arreaning common abla to modulate a make activity without and and host cell transformed with PRKAG3 or a sequence consisting of PRKAG3 or its mutant, are useful for arreaning cannot abla to modulate a make activity without and activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD03320
                                                                                                                                                                                                                                                              The present sequence is a cDNA encoding human adenosine monophosphate
                                                                                                                                                                                                                                                                                                                                                   New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment associated with energy metabolism such as diabetes, obesit
                                                                                                                                                                                                                                                                                                        Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
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18-MAY-2000; 2000EP-0401388
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LOOFT C.
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useful for acid
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Matches 101
                                                     New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
Claim 12; Fig 2; 71pp; English
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in a sequence of PRKAG3 and
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18-MAY-2000;
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Gellin
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Pred. No. 1.1e-22;
Mismatches 0;
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and
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(INRG ) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L.
                                                                  10-SEP-1999;
18-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                         Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorec genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                              22-MAR-2001.
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2000EP-0401388
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83.78;
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Pred. No. 1.3e-13;
0; Mismatches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                       Pig;
                                                                                         PRKAG3; diabetes;
genetic testing; c
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                                                                            cystathione
                                                                                                                                                    Sus scrofa
                                                                                                                                                                                                                                             AAD03321 standard;
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Iannuccelli N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 62-64;
                                                                                                                                                    PRKAG3 splice variant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                (first entry)
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, Gellin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP;
Location/Qualifiers
1..1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 A; 580 C;
                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.7%;
83.7%;
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                                                                                                                                                                                                                                             2022
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Pred. No. 1.3e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       535 G; 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Milan D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n D, Robic A,
Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1873;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                       anorectic;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                   468
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64 cagatctacatgcgcttcatgcaggagcacacctgcta 101

caggictacatgcacticatgcaggagcacacctgcta

656

4 tccccgcaggccccatttcccaagctgggctgggatgacgaactgcgggaaaccccggcgcc 63

0;

tccccagaggtgctgttacccaggctgggctgggatgatgagctgcagaagccgggggcc 618

559

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619

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AAS51418 AAS51418

DNA;

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CC kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice (C variant DNA. Prkag3 gene is located in the RN locus of chromosome 15. CC Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as CC diabetes, obesity, and disorders associated with muscle metabolism CC such as myopathy and cardiovascular diseases, to modulate AMPK CC activity, and for restoring a normal AMPK function. PRKAG3 sequence CC and its functionally altered mutants are useful for the diagnostic CC evaluation, genetic testing and prognosis of a metabolic disorder, CC preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are CC useful for detecting a dysfunction of carbohydrate metabolism resulting CC from the expression of a functionally altered allele of PRKAG3. CC Transgenic animal and host cell transformed with PRKAG3 or a tereoring compounds able to modulate AMPK activity. Nucleic acid concoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or of parkag3 are sequence encoding the first cystathione beta synthase (CBS) domain
                Query Match
Best Local Similarity
   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                           Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myopathy
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Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-SEP-2000; 2000WO-EP09896
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(ANDE/)
(LOOF/)
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18-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KALM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-2001
                                                                                                          PRKAG3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KALM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANDERSSON
 Conservative
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2000EP-0401388
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I, Gellin
                                                                                                        is useful in gene therapy.
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/product= "Sus scrofa Prkag3 splice variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 71pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAT RECH AGRONOMIQUE
                71.78;
83.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kalm
                                                                                                                                                                                                                                                                                                                                                                                                                                                  English
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-⊶ Roy
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                                                                                                                                                                                                                                                                                                                                                                                                     adenosine monophosphate (AMP)-activated muscle-specific isoform, PRKAG3 splice
0;
                Pred. No. 1
                              Score 72.4;
 Mismatches
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                .3e-13
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                                2022;
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Gaps
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CC Note: The sequence data for this patent did not form part CC of the printed specification, but was obtained in electronic CC format directly from WIPO at CC format directly from WIPO at
                                                                                                                     Matches
                                                           1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                         Sequence 1428 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; Seq ID No 4000; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIT-)
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22 - DEC - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2001
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                              63
                                                                                                                                 Local Similarity
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                                                                    9tccccgcaggccccatttccccaagctgggctgggatgacgaactgcgggaaacccgggcgc 62
gctgagcatcatgctgatcatgccggagcac 1308
               ccagatctacatgcgcttcatgcaggagcac 93
                                                   gttccgtatgtggctatatccctggctgacctgggcggtgatcctgttcatcgtcgccgc 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-611495/70.
                                                                                                                     53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds; prokaryotic
; antibacterial;
                                                                                                                   Conservative
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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Xu HH;
                                                                                                                                                                                      206 A; 525
                                                                                                                               29.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind
                                                                                                           Score 30.2; DE Pred. No. 3.2; 0; Mismatches
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                                                                                                                  0,
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                                                                                                                                                                                      274 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wall D,
                                                                                                                                             DВ
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64 cagatotacatgogottcatgoaggagoacacctg

tccccttatcccccatcctccctgctgaggtgtgtgggcgcacagcgcgggactggcggg 2769

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                                                                                                                                                   The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II) the polynucleotides are also used in diagnostics as expressed sequence tags of for identifying expressed genes. (I) is useful in gene therapy techniques (CI). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical (II) adjunctions of sites expressing (II). (I) and (II) are useful for treating considered involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO cx at ftp.wipo.int/pub/published_pct_sequences.
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AAS74198
                                                               Matches
                                                                                                                                                 Sequence 3918 BP; 1328 A; 872 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 10002; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS74198
                                                                              Local Similarity
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tccccgcaggccccatttcccaagctgggctgggatgacgaactgcggaaacccggcgcc 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-639362/73.
                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human diagnostic protein #10002
                                                                          29.1%;
                                                        Score 29.4; DB Pred. No. 6.9; 0; Mismatches
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                                                                                                                                                 822 G;
                                                                                                                                                 896 T; 0 other;
                                                                                               DB
                                                         41;
                                                                                         Length 3918;
                                                         Indels
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                                                      Gaps
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2770 cagctccacctgcagccccagtgcgagatccactg 2804

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                                                                                                                                                                                         cc polyniclectifes are also used in diagnostics as expressed sequence tags cf for identifying expressed genes. (I) is useful in gene therapy techniques ct to restore normal activity of (II) or to treat disease states involving cc (II). (II) is useful for generating antibodies against it, detecting or cc a food supplement. (II) and its binding partners are useful in medical cc imaging of sites expressing (II). (II) and (II) are useful for treating cc disorders involving aberrant protein expression or biological activity. Cc diagnostics, forensics, gene mapping, identification of mutations cc responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cd sequences. AAS64197-AAS94564 represent novel human cc specification, but was obtained in electronic format directly from WIPO car fire wire intended and references of the invention.
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AAS80424
                                                                             Matches
                                                                                          Query Match
Best Local Similarity
2710 tccccttatcccccatcctccctgctgaggtgtgtgggcgcacagcgcgggactggcggg 2769
                                                                                                                                                   Sequence 3918 BP; 1328 A; 872 C; 822 G; 896 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutatio responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biodiversity
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #16228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2002 (first entry)
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                    4 teccegeaggececattteceaagetgggetgggatgaegaaetgeggaaaeceeggegec 63
                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID No 16228; 103pp; English.
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0540217.
2000US-0649167.
                                                                                      29.1%; 56.8%;
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                                                                     Score 29.4; DB Pred. No. 6.9; 0; Mismatches
                                                                        0
                                                                                                    DB 23;
                                                                     41;
                                                                                                                                                 0 other;
                                                                                                  Length
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of mutations
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC in its in the control of the control
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AAS74446
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          Sequence 4397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and nolynestide (II) sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 10250; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002 (first entry)
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BP; 1506 A; 980 C; 935 G;
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2000US-0649167.
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  976 T; 0
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Query Match Best Local S Matches 54

Local Similarity

29.1%; 56.8%;

Score 29.4; Pred. No. 7; Mismatches

DB

Conservative

0;

41; 23;

Indels Length 4397;

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Gaps

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The invention relates to isolated polynucleotide (I) and CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC consistency of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC diagnostics, forensics, gene mapping, identification of mutations in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed control in the control control of the control of the
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AAS73340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding novel human diagnostic protein #9144
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                                      ftp.wipo.int/pub/published_pct_sequences.
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>B; ABG09153.
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Query Match

29.18;

Score 29.4;

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23;

Length 5122;

Sequence 5122 BP; 1815 A; 1151 C; 1032

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1124 T;

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RESULT

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ABL19505
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Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                                                                                                                   useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of discoticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLG177-ABB72072) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                       Sequence 1406
                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 9988; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
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11-JUL-2000;
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(PEKE ) PE CORP NY.
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                                                                               Conservative
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2000US-0614150
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                                                                                                                                                                    BP; 358 A; 409 C; 404 G; 235 T; 0 other;
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                                                                                              28.7%;
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                                                                                            Score 29;
Pred. No. 7
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                                                                             Mismatches
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                                                                                                             Length 1406;
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Best Local :
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                                                    Drosophila melanogaster genomic polynucleotide SEQ ID NO 9979.
                                                                                                                                                                                               1264
Drosophila melanogaster
                   Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
                                                                                                            ABL19502;
                                                                                    26-MAR-2002
                                                                                                                                 ABL19502 standard;
                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaccutical drugs. The invention discloses genomic DNA sequences (ABL018176-ABL30511), expressed DNA sequences (ABL018140, ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                        Sequence 3406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 9985; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC, Adams M,
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interactions
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                                                                                                                                                                                                  49 cggaaacccggcgcccagatctacatgcgcttcatgcaggagcacacctgcta 101
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                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                          Conservative
                                                                                (first entry)
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2000US-0614150
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                                                                                                                                 3593
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                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLG1840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                            Sequence 3593 BP;
                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 9979; 21pp + Sequence Listing; English.
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A1106144 db03d12_p
BE540087 601060879
B1199916 602760950
BH140228 ZMMBBD000
AL150666 Anopheles
AL212510 Tetraodon
BM13818 NXLV_012_
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JOURNAL MEDLINE COMMENT ACCESSION VERSION KEYWORDS RESULT 1
BF890374
LOCUS
DEFINITION REFERENCE AUTHORS SOURCE ORGANISM FEATURES TITLE source Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013
Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
Fax: 402 762 4390 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and FORMARD: AGGADACAGCTATGACCAT BACKMARD: GTTTTCCCAGTCACGACG Plate: 57 row: H column: 11 Seq primer: ATTTAGGTGACACTATAG PCR PRimers Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; BF890374 444 bp mrNA linear 291826 MARC 3BOV Bos taurus cDNA 5', mRNA sequence. BF890374 BF890374.1 GI:12281760 EST. Keele, J.W. Bovidae; Bovinae; Bos. Bos taurus (bases 1 to 444) -minmatch 12 options. /organism="Bos taurus" /db_xref="taxon:9913" Location/Qualifiers cross_match with the -minscore EST 25-APR-2001 ; ; 18

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467815 MA
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Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Email: spith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
Single pass sequencing bases called and alt_trimmed with phred
200.980904.e. Vector identified by cross_match with the -minscore 18
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PO Box 166, Clay Center, NE 68933-0166, USA
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                                   ø
                           /tissue_type="pooled"
/lab_host="DHIOB"
/lab_host="DHIOB"
/note="Vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;
/note="Vector: pcmV SPORT6; 
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147 c 139 g 67 t
                                                                                                                                                                                                                                                                                /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
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/tissue_type="pooled"
/lab_host="DH10B"
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Pred. No. 7.5e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gsc.riken.go.jp,
URU:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1650 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
hayashizaki,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute Ohysical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Koud, M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasak,D., Shibatta,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
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                                                                                                                                                                                     Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizaw,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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83; Conserv
                                                                              Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                      RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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e mouse tissues.
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,Y. and Hayashizaki,Y.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with tuman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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Location/Qualifiers
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Pred. No. 7.9e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCCCACAGGCCCCACTTCTTGGCCTGAGTTGGGATGACCAACTTCACAAACCCGGAGCC 555
                                           Fax: 61//20000
Email: fishman@mgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
The original clones used for sequencing are no longer available;
                                                                                                                                      Expressed Sequences from The Adult Zebrafish Heart Unpublished (1998)
Contact: Mark C. Fishman
Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, 1
                                                                                                                                                                                                                                                       Chen, J.N., DeSauvage, F., Hosobuchi, M., Jackson, D.G. and Fishman
                           the library is available Insert Length: 326 Std Seq primer: pl
                                                                                                                                                                                                                                                                                        Actinopterygii; Ncopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Site_1: SalI; Site_2: BamHI; cDNA library
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/lab_host="DH10B"
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/db_xref≈"taxon:10090"
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COMMENT

Matches Query Match

Local Similarity

30.3%; 62.3%;

Pred. No. 68 0; Mismatche

68

DB 10;

Length Indels

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Mismatches

29;

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SOURCE

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BE540087/c
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                                                                                                                                                                                                                  High quality sequence stop: 668
Location/Qualifiers
                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 679)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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            a
         /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."

a 226 c 177 g 152 t
                                                                                                  /lab_host="DH10B"
                                                                                                              /clone_lib="NIH_MGC_10"
/cell_line="MGC36"
                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="E. coli xLl Blue"
/note="Organ: heart; Vector: LambdaZAPII; Site_1: EcoR1;
Site_2: xhol"
a 66 c 96 g 79 t 2 others
                                                                                                                                               /clone="IMAGE:3447378"
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/clone_lib="ZF adult heart library"
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/strain="AB"
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62.78;
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Plate: LLCM/783 row: c column: 13
High quality sequence start: 5
High quality sequence stop: 669.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/
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BI199916
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Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:496324"
/clone_lib="NIH_MGC_19"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/lab_bost="DH10B (phage-resistant)"
/la
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sapiens cDNA clone IMAGE:4896324
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DEFINITION
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Best Local
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100 Jordan Hall, Cl
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                 Anopheles gambiae
Eukaryota; Metazoa
Pterygota; Neopte
                                                                                                                                                                                                                                                                                                                                                                                                                       CNS01MA1 894 bp DNA linear GSS 14-JUN-200: Anopheles gambiae GSS SP6 end of clone 21E19 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),
Genoscope
                                                                               Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence.
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                                                                                                                                                                                                                                  African malaria mosquito.
                                                                                                                                                                                                                                                                                                                      AL150666.1 GI:7011145
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Zea mays
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High quality sequence stop: 510
Location/Qualifiers
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Class: BAC ends
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47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University Genomics Institute
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//lab_host="E. coli"
/note="Vector: pcUGIBAC-1; Site_1: HindIII; Site_2: NotI;
/note="Vector: pcUGIBAC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="ZMMBBb0001L18f"
/clone_lib="Maize B73"
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                                                                                                        Neoptera; Endopterygota; Diptera; Nematocera;
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                                                                                                                                              Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                        Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
                                                                                                                                                                              Roest Crollius, H., Jaillon, O., Dasilva, C., Boune Bernot, A., Fizames, C., Wincker, P., Brottier, P., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                     Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL212510.1 GI:7871329
GSS: genome survey sequence.
Tetraodon nigroviridis.
                                                                              Direct Submission
                                                                                                                                   Unpublished
                                                                                                                                                      Tetraodon nigroviridis
                                                                                                                                                                       Human gene number estimate
                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                Bouneau, L., Billault, A., Weissenbach, J.
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Bouneau,L., Billault,A., Quetier,F., Sauri
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163G17 of library G from Tetraodon
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Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue d
Roux, Paris 75015, France

This clone is from an A. gambiae BAC library provided by
Collins and sequenced by Genoscope in collaboration with
Laboratory of Biochem. and Biol. Molec. of Insects, Insti
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Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pasteur.
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/clone="21E19"
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/strain="PEST"
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Saurin,W., Bernot,A. and
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Quetier,F.,
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                                                                                                                                                     Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ dat
This sequence is a single read and was generated as
scale clone-end sequencing project of the Tetraodon
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                     Roest-Grollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using Tetracdon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                            Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi, Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL233007.1 GI:7892142
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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Tetraodon nigroviridis genome survey sequence T7 end of clone
005N22 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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Roest-Crollius, H., J
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   /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="005N22"
/clone_lib="G"
/note="Genoscope sequence ID : COBG005DG11xD1-end :
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/clone="163G17"
/clone_lib="G"
/note="Genoscope sequence ID : COAC
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          BE269692 930 bp
601185836F1 NIH_MGC_8 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              North Carolina State University Tel: 919 515 7800 Fax: 919 515 7801 Email: ajohnson@unity.ncsu.edu Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Johnson, Arthur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; 1 (bases 1 to 655)
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BM133818.1 GI:17141057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pTriplEx; Site_1: EcoRI; The library is from late (summer August) wood, taken from below the crown of a 20 year old tree. The harvested xylem tissue was on the the cusp between transitional and mature wood. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGCCATTATGGCC'."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="NXLY_012_F09"
/clone_lib="NXLV (Nsf Xylem Late wood Vertical)"
/tissue_type="primary xylem"
/dev_stage="late wood"
/lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
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Pred. No. 1.3e+02;
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          mRNA linear EST 13-JUL-2000 CDNA clone IMAGE:3543584 5',
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Pinus; Pinus.
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                       NIH-MGC http://mgc.nci.nih.gov/.
national Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae.

1 (bases 1 to 955)
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                 mRNA sequence.
BG394974
BG394974.1 GI:13288422
EST.
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602457369F1 NIH_MGC_16 Homo sapiens
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
plate: LLCM237 row: g column: 09
High quality sequence stop: 238.
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Contact: Robert Strausberg, Ph.D.
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BE269692
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 930)
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: DOTB7; Site_2: DOTB7; Site_3: Note of Site_3: Note of Site of Si
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/clone_lib="NIH_MGC_8"
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/db_xref="taxon:9606"
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Pred. No. 1.4e+02;
0; Mismatches 39;
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s cDNA clone IMAGE:4579696 5',
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BM468546
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Watches 42; Conserve
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                                                                                                                                                                         cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM1232 row: m column: 09 High quality sequence stop: 725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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5', mRNA secuence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="relinoblastoma"
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/lab_host="Phage-resistant]"
/lab_host="Phage-resistant]"
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/lab_host="Phage-resistant]"
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/lab_host="Phage-resistant]"
/lab_host="Phage-resistant]"
/lab_host="Phage-resist
                                                                  /organism="Homo sapiens"
/clone="IMAGE:5578160"
                                   /db_xref="taxon:9606"
                                                                                                                                         ocation/Qualifiers
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/db_xref="taxon:9606"
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Pred. No. 1.6e+02;
""" matches 21;
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                                                                                                                                                                                                                                                                                                                                                                       One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Blast expect value = 1.1E-117 on X03121: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harvey,D., Brokstein,P., Hong,L.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins.
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 313)
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Lawrence Berkeley National Lab
Berkeley, CA 94720, USA
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LD08544.Sprime LD Drosophila
Drosophila melanogaster cDNA
AA264931
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Similarity 64.2%;
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          72
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/note="Organ: embryo; Vector: BlueScript SK; Site_1: EcoRI
; Site_2: XhoI; Constructed using Stratagene ZAP-cDNA
Synthesis klt. Oligo dT-primed and directionally cloned at
EcoRI and XhoI in BlueScript SK(+/-)*
                                                                                                   /clone_lib="LD Drosophila melanogaster embryo BlueScript"/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
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/db_xref="BBGP_EST:BDC1n007879"
/db_xref="taxon:7227"
/clone="LD08544"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="organ: skin: Vector: pcMY-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
303 g 174 t 3 others
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Pred. No. 1.9e+02;
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Query Match

Local Similarity

28.7%; 71.7%;

Score 29; l Pred. No. 1.

DB 9; .6e+02; es 15;

Length 313;

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Result
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3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

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Match Length DB
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US-08-804-198-1
4 US-09-103-80A-2
US-08-441-507-17
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US-08-463-909B-13
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Sequence 7, Appli
Sequence 2, Appli
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Sequence 17, Appli
Sequence 17, Appli
Sequence 13, Appl
Sequence 14, Appl
Sequence 40, Appl
Sequence 47, Appl
Sequence 46, Appl
Sequence 47, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 52, Appl
Sequence 1, Appli
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	23.6	23.6	23.6	23.8	24.0	24.0	24.0	24.0	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2
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ALIGNMENTS

CDS 14046
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EY: CDS
EY: CDS
LOCATION: 35014002
CDS
MOLECULE TYPE: DNA (genomic)
пe
DEDNESS:
nucleic acid
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SEQUENCE CHARACTERISTICS:
EOB SEO ID NO:
ATTON INFORMA
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ON NUMBER: 35,784
, Thomas,
Y/AGENT I
ON: 435
ar
APPLICATION NUMBER: US/08/804,227C
LICATION DATA:
ASCI (DOS
OPERATING SYSTEM: MS-DOS
7
READABLE FORM
46285
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INDIANAPOLIS
ILLY CORPORATE CENTE
ADDRESSEE: THOMAS G DIANT 1501
NIMBER OF SECTION: POLYKETIDE SYNTHASE
CANT: Sutton, Kimberly L.
Rosteck, Paul R.
Kuhstoss, Stuart
GENERAL INFORMATION:
ce 7,
227C-7
RESULT 1
FOIL D 1

FEATURE

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FEATURE:

NAME/KEY:

LOCATION:

US-08-804-227C-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27484 CCGCTGCTGGGCAGCGGCGTCGAACTGCCGGAGTCCGGTGACCGGATGTACA 27535
                                                                      NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELI. 11
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Burgett, Stanley G.
APPLICANT: Kubstoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATEROLIDE SYNTHASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Macintosh 7.0 SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
                                                                                                                                                           LOCATION: FEATURE:
                                                                                                                                                                                                      MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
                              FEATURE:
                                                                                                                   FEATURE:
 NAME/KEY:
                                         NAME/KEY:
                                                                                                                                                                                                                                            LENGTH: 44377 base pairs TYPE: nucleic acid STRANGEDNESS: single
                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/804,198 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: INDIANAPOLIS STATE: IN
                                                                                                                             LOCATION:
                                                                                                                                              NAME/KEY:
                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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nes 36; Conserv
                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 cccaagctgggctgggatgacgaactgcggaaacccggcgcccagatctaca 73
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36155..41830
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31329..36071
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Pred. No. 17;
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; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
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                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Singh, M
APPLICANT: Smith, F
APPLICANT: Knox, Rc
                                                                                                                                                                                                                                                                                            Sequence 17, Appli Patent No. 6214358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             2113630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 4403765

TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                     NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD LLP
                                                                                                                                                                                   TITLE OF INVENTION: Protein A
                                                                                                     CITY: Boston
                                                                     COUNTRY:
                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                   66 gatctacatgcgcttcatgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 cccaagctgggctgggatgacgaactgcggaaacccggcgcccagatctaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 cccgcaggccccatttcccaagctggggtggggatgacgaactgcgggaaacccgggcgcca 65
                                                                                                                                                                                                                                                                                                                                                                                        gaaccggatggtcagctggc 2113649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47;
                                                        02109
                                                                                      Massachusetts
                                                                                                                                                                                                                                                                                                            Application US/08441507
                                                                                                                     28 State Street
                                                                                                                                                                                                                   Singh, Mohan Bir;
Smith, Penelope; and
Knox, Robert Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.7%;
58.8%;
                                                                                                                                                                                                      Protein Allergens
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69.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26; DB
Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                      of the
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                                                                                                                                                                                                      Species
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CURRENT APPLICATION DATA:

US/08/441,507

OPERATING SYSTEM: PC SOFTWARE: ASCII text

PC-DOS/MS-DOS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 727-7400
TELEPAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09029603 Patent No. 6210935
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Best Local :
                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            APPLICANT: Pospiech, Andreas
TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
FILE REFERENCE: 4-20555/A/PCT
CURRENT APPLICATION NUMBER: US/09/029,603
CURRENT FILING DATE: 1998-03-20
EARLIER APPLICATION NUMBER: PCT/EP96/03643
EARLIER FILING DATE: 1996-08-19
NUMBER: OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schupp, Thomas
APPLICANT: Engel, Natalie
APPLICANT: Bietenhader, Jurg
APPLICANT: Toupet, Christine
                                                        OTHER INFORMATION: ORF FEATURE.
                                                                                   NAME/KEY: misc_RNA
LOCATION: (1747)...
                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Streptomyces longisporoflavus
LOCATION: (2593)..(4011)
OTHER INFORMATION: ORF
                   NAME/KEY: misc_RNA
LOCATION: (2593)...
                                                    FEATURE:
                                                                                                                                            NAME/KEY: misc_RNA
LOCATION: (378)..(1665)
OTHER INFORMATION: ORF
                                                                                                                              FEATURE:
                                                                                                                                                                                                   FEATURE:
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FILING DATE: 30-October-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras. Amv F
                                                                                                                                                                                                                                                         ENGTH: 6085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 594 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 15-May-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 cgcaggccccatttcccaagctgggctgggatgacgaactgcggaaaccccggcgcccaga 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTTCGGCGCCATGGCCAAGAAGGGCGAGGAGGACAAGCTGCGCAAGGCCGGCGAGCTGA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity 63.9
39; Conservative
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Pred. No. 9.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNIN.
ZIP: 90071
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: TBM PC compatible
TOWNITER: TBM PC compatible
TOWNITER: TBM PC compatible
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Best Local
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APPLICATION NUMBER: US/08/463,081B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
ANABE: VIVIANA AMZEJ, Ph. D.
REFERENCE/DOCKET NUMBER: 20,930
REFERENCE/DOCKET NUMBER: P66 38150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                            TELEFAX: (213) 489-42 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_RNA
LOCATION: (5071)..(6085)
OTHER INFORMATION: ORF
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NAME/KEY: misc_RNA
LOCATION: (4013)..(4999)
OTHER INFORMATION: ORF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 444 CONTROL OF CITY: LOS Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3243 ccgctggctcaccctcggccagatcgccgaactgctgcacgaggacgacctggtcaacat 3302
                                                      TOPOLOGY: li
                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereo
                                         FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compati
OPERATING SYSTEM: PC-DOS
SOFTWARE: PatentIn Relea
SOFTWARE: Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 25.5%;
Local Similarity 56.5%;
                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: PRETTY, SCHROEDER & POPLAWSKI 444 South Flower St. - Suite 1900
                                                                                                                                  2980 base pairs
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                                                                            linear
                                                                                                                                                                                             489-4210
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                                                                                                                                                                                                                                                       P66 38150 (DART-060)
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Pred. No. 17;
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US-08-462-390B-13/c
                                RESULT
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; LOCATION:
US-08-461-379A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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Best Local S
Matches 33
                                                                                                                                                                                                                                                                            Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 27-OCT-1994; 10-ATTORNEY/AGENT INFORMATION:
NAME: VIVIANA AMZEL, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: TOTAL STATES OF THE 
                                                                                                                         2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS
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TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
TITLE OF INVENTION: Expression Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentID Release #1.0, SOFTWARE: Version #1.25
                                                                                                                                                                                                                                            Local Similarity
nes 33; Conserv
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nes 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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    Application US/08461379A
5871961

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240..1475
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71.7%;
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71.7%;
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                                                                                                                                                                                                                                         Score 25.2; D. Pred. No. 22; 0; Mismatches
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Pred. No. 22;
0; Mismatches
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                                                                                                                                                                                                                                         13;
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US-08-463-074B-13/c
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                                                                                                                                                                                         Sequence 13, Application US/08463074B Patent No. 6020155
                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 71.7%; Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/08462390B Patent No. 5882894
                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (610)407-070 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Viviana Amzel, Ph. D. REGISTRATION NUMBER: 30,930 REFERENCE/DOCKET NUMBER: DANTELECOMMUNICATION INFORMATION: TELEPHONE: (610,407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
                                                                                          NUMBER OF SEQUENCES: 3
                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                          2119 TTCCGAGGCAGGGGTGGGGAGCCAGACCTGCGGGAAACCCTCCCCCAA 2074
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FEATURE:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                         APPLICANT:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               20 ttcccaagctgggctgggatgacgaactgcggaaacccggcgccca 65
              CITY: Los Angeles
STATE: California
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LOCATION: 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Valley Forge
STATE: Pennsylvania
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ADDRESSEE: . (B) STREET:One Westlakes-Berwyn
COUNTRY:
                                                        ADDRESSEE:
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                                                                            ADDRESSEE:
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nucleic acid
USA
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VENTION: Nucleic Acids Encoding CR8 Polypeptide, V
VENTION: Transformed Cell Thereof, and Expression
                                                                                                                                                     Smith, Kendall A. & Beadling, Carol
                                                                        PRETTY,
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                                                                                                                                 Nucleic Acids Encoding
                                                      SCHROEDER & POPLAWSKI
(B) STREET:
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Pred. No. 22;
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                                                                                                                                 CR1 Fusion Protein, Vector an
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ATTORMET/AGENT INFORMATION:
NAME: VIVIANA AMZE1, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION NOTA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
TITLE OF INVENTION: Transformed Cell Thereof, and Expression There
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
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MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Local Similarity 71.7%;
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LOCATION:
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ZIP: 900071
                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: Californiaa
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Pred. No. 22;
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2980 base pairs
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NAME/KEY:
LOCATION:
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SOFTWARE: Version #1.2
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
                PRIOR APPLICATION DATA:
                                                            FILING DATE: 5-JUN-1 PRIOR APPLICATION DATA:
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NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                        APPLICATION NUMBER: EP /
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/
                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
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                              FILING DATE:
                                             APPLICATION NUMBER:
                                                                                                                                                                           FILING DATE: 5-JUN-1996
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                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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33; Conserv
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Version #1.25
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                               5-JUN-1995
                                                                           JMBER: 08/463,074
5-JUN-1995
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20-NOV-1991
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Nucleic Acids Encoding CR5

Polypeptide, Vector and Transformed Cell Thereof, and

Expression Thereof
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71.7%;
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08/462,390
                                             08/462,337
                                                                                                                                                                                                                     EP App. # 96921319.8
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Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 2980;
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Suite

5-JUN-1995

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Query Match
Best Local Similarity
"~* hes 53; Conserv?
                                                                                                 ; NAME/KEY: modified base
; OTHER INFORMATION: n rep
US-08-990-823-31
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; LOCATION:
US-08-652-446-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-990-823-31
                                                                                                                                                                                              SOFTWARE: PatentIN Ver. SEQ ID NO 31 LENGTH: 255
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/08990823D Patent No. 6228371
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                         APPLICANT: Nano, Francis

TITLE OF INVENTION: immunostimulatory Peptides

FILE OF INVENTION: immunostimulatory Peptides

FILE REFERENCE: 49086

CURRENT APPLICATION NUMBER: US/08/990,823D

CURRENT FILING DATE: 1997-12-15

EARLIER APPLICATION NUMBER: US 96/10375

EARLIER FILING DATE: 1996-06-14

EARLIER FILING DATE: 1995-06-15

NUMBER: 05-06-15

NUMBER: OF SEO, ID NOS: 113

COURTER OF SEO, ID NOS: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local :
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FILING DATE: 5-UN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: VIVIANA AMZEL, Ph. D.
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2119 TTCCGAGGCAGGGGTGGGGAGCCAGACCTGCGGAAACCCTCCCCCAA 2074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 5-JUN-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 ttcccaagctgggctgggatgacgaactgcggaaacccggcgccca 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/463,081 FILING DATE: 5-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                 Conservative
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71.7%;
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                              Score 24.8;
Pred. No. 17
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Pred. No. 22;
                                                                                                               a or
               Mismatches
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                                            DB 4;
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               47;
                                            Length 255;
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RESULT 14
PCT-US93-06251-65/c
Sequence 65, Application PC/TUS9306251
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLE
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US
FILING DATE: September
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lin
                                                                                                      469 CTGCTCCAGCTCCATGTGGCGGTAGAGCTGCT 438
                                                                                                                                                                       529 GGAGACCTGGTGGCCAAGACTGGGATGGGGTGGCACCATGGGGGGTATCGAGGACGTGCAT 470
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                                                                                                                           69 ctacatgcgcttcatgcaggagcacacctgct 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PS,
OPERATING SYSTEM:
                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Penn Control Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 cccagatctacatgcgcttcatgcaggagcacacctgcta 101
                                                                                                                                                                                         9 gcaggccccatttcccaagctgggctgggatgacgaactgcggaaacccggcgcccagat 68
                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                             1364 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Seidel, Gonda, Lavorgna & Monaco,
Two Penn Center, Suite 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette, 3.50 inch, 720
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N: 514
                                                                                                                                                                                                                                                       24.6%;
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OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MS-DOS
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ber 15, 1994
                                                                                                                                                                                                                                       ; Score 24.8; D; Pred. No. 25; O; Mismatches
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APPLICANT:

Wickstrom, Eric and Rife, Jason

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GENERAL....

APPLICANT: Mulero, Julio
APPLICANT: Weung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO (
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO (
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36570
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-09-608-285A-47/c
: Sequence 47, Application US/09608285A
: Patent No. 6335013
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: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 50; Conserv
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MIDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US93/06251
FILING DATE: 1930630
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 GGAGACCTGGTGGCCAAGACTGGGATGGGGTGGCACCATGGGGGGTATCGAGGACGTGCAT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 ctacatgcgcttcatgcaggagcacacacctgct 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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Stereospecific Alkylphosphonates and Arylphosphonates
93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 24.8; D; Pred. No. 25; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8586
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                                                                                                                                                                                                         ; LENGTH: 1900
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-47
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                                                                                                                                                                                                                                                                         SOFTWARE: SEQ ID NO 47
                                                                                                                           Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1998-07-16
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1999-02-04
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1999-07-09/
PRIOR APPLICATION NUMBER: 09/
491
                                                            551 CTGTGTCTCCAGGGTCCGACACACGTACTTGGCTGCGATCTCGAAGTCCCCCACCACCAG 492
               61 gcccagatctacatgcgcttcatgcaggagcacacctgct 100
                                                                               1 ctgtccccgcaggccccatttcccaagctgggctgggatgacgaactgcggaaacccggc 60
GCTGCCTCCCTTCTCCGCATCTATGAGGCCCACACCAGCT
                                                                                                                                                                                                                                                                                          PatentIn Ver. 2.0
                                                                                                                             Conservative
                                                                                                                                          24.6%;
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                                                                                                                                                                                                                                                                                                                                           09/118,205
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                                                                                                                         Score 24.8; DE Pred. No. 27; 0; Mismatches
                                                                                                                           0;
                                                                                                                                                           DB 4;
                                                                                                                         47;
452
                                                                                                                                                         Length 1900;
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AX099800
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AJ249977 Homo sapi

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AX281580 Sequence

AX281580 Sequence

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Andersson,L., Luthman,H. and Markiu
Variants of the human amp-activated
Patent: WO 0177305-A 5 18-OCT-2001;
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Sequence 5 from Patent I
AX281582
AX281582.1 GI:16608833
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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20. 1489
                                                                                    Location/Qualifiers
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REFERENCE
AUTHORS
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SOURCE
ORGANISM
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Sequence 3 from Patent W00120003
AX099776
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Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A. Rogel-Gaillard, C., lannuccelli, N., Gellin, J., le Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Vertebrata;

Euteleostomi;

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mRNA, complete cds.
AF214519
AF214519.1 GI:8215681
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata;
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Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
1. .2115
                                    human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 2115)
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AVVLETAPILTALDIFVDRRVSALPVNNCCGOVVGLYSRFDVIHLAAQOTYNHLDMSV
GEALRORTLCLEGVLSCOPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA"

4 622 c 562 g 471 t
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/db_xref="GI:13538837"
/db_xref="GI:13538837"
/db_xref="GI:13538837"
/translation="MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEG
EPPGQEEGPRSRFTARSTGLEATFPKTTPLAQADPACVGTPPTGMDCLPSDCTASAAG
SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
RFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFYGMLTI
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                              Score 101; DB 6
Pred. No. 1e-20;
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                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedis University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                   AMP-activated
                                                                                                                                                       HSA249977
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Science 288 (5469), 1248-1251 (2000)
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//COGOO_Start=1
//Protein_id="AMP-activated protein kinase gamma subunit"
//protein_id="AAF73987.1"
//protein_id="AAF73987.1"
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ESTDDVELATEFPATFAWECELEGLLEERPALCLSPQAFFKLGWDDELRKPGAQIYM
RFMQEHTCYDAMATSSKLVIFOTMLEIKKAFFALVANGYRAAPLWDSKKQSFVGMLTI
TDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLI
KNRIHRLPVLGPVSGNVLHILTHKRLLKFLHIFGSLLPRRSFLYXTIQDLGIGTFRDL
AVVLETAPILTALDIFVDRRYSALPVNUECGQVVGLYSRFDVIHLAAQQTYNHLDMSV
GEALRORTLCLEGVLSCQPHESJGEVIDRIAREQVHRLVDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA"
ALVLSPAGIDALGA"
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/db_xref="taxon:9606"
/chromosome="2"
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Eukaryota;
Mammalia; E
same, and uses thereof
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT MATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
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                                                                                                           1 (bases 1 to 1867)
Andersson,L., Looft,C., Kalm,E., Milan,D., Rojen-Gaillard,C., Iannuccelli,N., Gellin,J.,
                                                                                                                                                                                                                                                                                     Sequence 1 from AX099774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (12-OCT-1999) Carling D., Cellular Stress Group, M Clinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 ONN, UNITED KINGDOM
                                                                        Variants of the gamma chain of ampk, dna sequences encoding
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/product="AMP-activated protein kinase gamma 3 subunit"
/protein_id="CAMS5117.1"
/db_xref="G1-6688201".
/translation="MEDGLEHALERTPSWSSLGGSEHOEMSFLEQENSSWPSPAYTS
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DPAGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALC
LSPQAFPKLGWDDELKRCAQ1YMRFLEEHTCYDAMATSSKLV1FDTYMLEIKAFFFA
LVANGVRAAPLMDSKKOSFVGWLT1TDFILVLHRYFRSPLVO1YEIEDHKIETWFEIF
LVANGVRAAPLMDSKKOSFVGWLT1TOFILVLHRYFRSPLVO1YEIEDHKELLKFLHFFLHIF
LOGGCKRPLVSISPNDSLFEAYYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHFFLHIF
LOGGCKRPLVSISPNDSLFEAYYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHFF
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VGLYSRFDVIHLAAQQTYNHLDMSVGEALRKRTLCLEGVLSCQPHESLGEV1DR1ARE
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22. .1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="AMPK gamma 3"
/function="AMP-activated
                                                                                                                                                                     Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Cetartiodactyla; Suina; Suidae;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                   GI:13538808
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                                                                                                                                                                                                                                                                                                  1867 bp
Patent W00120003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 101; DB 9;
Pred. No. 1e-20;
; Mismatches 0;
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J., le Roy,P.
                                                                                                                                                                       Euteleostomi;
Sus.
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   (FR);
Ernst (DE)
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                                                                                                                                                             Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics,
University of Agricultural Sciences, BMC box 597, Uppsala
                                                                                                                                                                                                                        2 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
proof Conference
                                                                                                                                                                                                                                                                                                                           skeletal muscle
Science 288 (5469), 1248-1251 (2000)
                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Sus scrofa
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mutation in PRKAG3 associated with excess glycogen content in pig
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/POODING TO A CACASTYSE A CACASTYSE A CACASTY ALVANGVRAAP
/LIANS LA LION "MHEMQEHEY VENDELVOIYELEEHK LETWREIY LOGCEKPLVS
LIMDSKKOSFVOKMLT ITOP FILVLHRY YESPLVOIYELEEHK LETWREIY LOGCEKPLVS
ISPNDSLFEAVYALIKNR IHRLPVLDPVSGAVLHILTHKRLLKFLHIEGTLLDRPSFL
VRT 10DLG 1GTFRDLAVVLETAP ILTALDIF VDRRVSALPVVNETGOVVGLYSREDV I
HLAAQOTYNHLDMNVCEALRORT LCLESVLSCOPHETLGEVIDRIVREQVHRLVLVDE
TOHLLGVVSLSDILQALVLSPAGIDALGA"

583 c 529 g 375 t
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/db_xref="taxon:9823**
472. .1389
                                                                            /organism="Sus scrofa"
/db_xref="taxon:9823"
/chromosome="15"
                                                                                                                              Location/Qualifiers
1. .1873
                               /tissue_type="skeletal muscle"
1. .1873
            'gene="PRKAG3"
                                                              'map="15q"
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Pred. No. 1.9e-18;
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62 atccaagatttgggcatcggcacattccgagacttggctg 101
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Sequence 27
AX099800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           same, and uses thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
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mmalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
(bases 1 to 1873)
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ALVLSPAGIDALGA"
580 c 53
                                                                                                                                /protein_id="CAC35800.1"
/db_xref="GI:13538835"
/db_xref="GI:13538835"
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GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
GSNTDHIDDGIEFSASAASGDELGLVEEKAFPALVARGVRAAPLWDSKKQSFYGNTI
HFMQDHTCVDAATSSKLVIFDTMLEIKKAFPALVARGVRAAPLWDSKKQSFYGNTI
TDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISPNDSLFEAVYALI
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GPPGPREGPQSRPVAESTGOEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
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TDFILVLHRYYBSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISPNOSLFEAVYALI
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TDFILVLHRYYBSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISPNOSLFEAVYALI
                                                                          KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
AVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
                                                  GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
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ALVLSPAGIDALGA"
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AVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
                                                                                                                                                                                                                                                                                                                                                                /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Sus scrofa"/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                     codon_start=1
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/codon_start=1
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from Patent W00120003.
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Pred. No. 1.9e-18;
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Ernst (DE)
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                                                                                                          TITLE
                                                                                                                                                                                                   ORGANISM
                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                    1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             967 ATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCCG 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 atccaagatttgggcatcggcacattccgagacttggctg 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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                                                                                                                                                                                                                                                                             Sequence 3 from Patent WO0177305 Ax281580
                                                                                                                                                                                                                                                                                                                    AX281580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AX099804
Sequence 31 from Patent
AX099804
                                                                                Variants of the human amp-activated protein kinase gamma 3 subunit Patent: WO 0177305-A 3 18-OCT-2001;
                                                                                                                    Andersson, L., Luthman, H. and Marklund, S
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                           AX281580.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent: WO 0120003-A 31 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variants of the gamma chain of ampk, dna sequences encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AX099804.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           same, and uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mmalia: Eutheria: Cetartiodactyla: Suina; Suidae: (bases 1 to 2022)
                                                                                                                                            (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          412
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                                                                AB (SE)
                            Location/Qualifiers
1. .1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Sus scrofa"
/db_xref="taxon:9823"
623 c 593 g
        /organism="Homo sapiens"
                                                                                                                                                                                                                                                           GI:16608831
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96.0%;
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WO0120003.
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                                                                                                                                                             Hominidae;
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                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                  PAT 03-NOV-2001
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Ernst
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AUTHORS
TITLE
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SOURCE
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AC027416/c
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ORIGIN
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Best Local
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                                                                                                                                                                                                         Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 7, 2000 this sequence version replaced gi:7342115. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, Y., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoia; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 152129)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-504G11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC027416 152129 bp
Homo sapiens clone RP11-504G11,
                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                    Center code: WIBR
                                                                                                                                                  Center: Whitehead Institute/ MIT Center
                                                                                                                Web site: http://www-seq.wi.mit.edu
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504 c 534 g
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91.3%;
Summary Statistics vector: M13; M77815;
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Pred. No. 4.9e-14;
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  100%
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Euteleostomi;

HTG

07-JUN-2000 32

of reads

for Genome Research

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100 bp
42366: contig of 4087 bp
42367 42466: gap of 100 bp
42467 46365: contig of 3899 bp 1
46366 46465: gap of 100 bp
46466 51285: contig of 4820 bp 1
51286 51385: gap of 100 bp
51286 55877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 135376 bases at least Q40
Consensus quality: 143364 bases at least Q30
Consensus quality: 146503 bases at least Q20
                                                                                                           7318: gap of 100 bp 73319 77115: contig of 3797 b 77116 77215: gap of 77216
                                                                                                                                                                                    60596 60695: gap of 100 bp 60696 66595: contig of 5900 bp in 66596 66695: gap of 100 bp 66696 73218: contig of 6523 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12557 12656: gap of 100 bp
12657 15043: contig of 2387 b
15044 15143: gap of 100 bp
15144 17123: contig of 1980 b
17124 1723: gap of 100 bp
                                                                                                                                                                                                                                                                                                                   55872
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1006 1105: gap of 100 bp
1106 2402: contig of 1297 bp
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60595: con+
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7547: r
                                                                              85122:
                                  93414:
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38179: contig of 4111 bp
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7647: gap of 100 bp
9983: contig of 2336 bp
10083: gap of 100 bp
12556: contig of 2473 bp
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5020: con
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3823: co
  414: gap of :
101193: contig of
                                                22: gap of 100 bp
93314: contig of 8192 bp in
                                                                                            215: gap of 100 bp 85022: contig of 7807 l
                                                                                                                                                                                                                                                                                                            385: gap of 100 bp
55871: contig of 4486 bp in
371: gap of 100 bp
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19466: contig of 2243 b
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contig of 1321 bp in length
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85123. .93314
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77216. .85022
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42467. .46365
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                                                                                                                                                                                                                      Sequencing vector: M13, 98%
Sequencing vector: plasmid; 0%
Sequencing vector: plasmid; 0% of reads
Chemistry: Dye-primer ET; 98% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: phrap; version 0.990319
Consensus quality: 187795 bases at least Q40
Consensus quality: 190513 bases at least Q30
Consensus quality: 190513 bases at least Q20
Consensus quality: 192099 bases at least Q20
Insert size: 200000; agarose-fp
Insert size: 194954; sum-of-contigs
Quality coverage: 5.58 in Q20 bases; sgarose-fp
Quality coverage: 5.57 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: H_NH0647005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Feb 21, 2001 this sequence version replaced gi:8469048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 196554)
Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence of Homo sapiens clone 
Unpublished
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HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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   1157: contig of 1157 bp in length 1257: gap of unknown length 3600: contig of 2343 bp in length 3700: gap of unknown length 5103: contig of 1403 bp in length 5203: gap of unknown length
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92241. .113337
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44743. .58275
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149388. .196554
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130426. .149287
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113438. .130325
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28988. .35255
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11957. .15783
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/chromosome="2"
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22007. .28887
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/note="assembly_name:Contigl8"
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                                                                                                                                                                                                                       Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Nov 8, 2001 this sequence version replaced gi:13431203.
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                                                                                                    Web site: http://genome.wustl.edu/gsc
contact: sapiens@watson.wustl.edu
-------Summary Statistics
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. I MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc Louis

donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-4705. Actual start of this clone is at base position 1 of RP11-459I19; actual end is at base position 206854 of RP11-459I19.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 AC009974. A single plasmid region exists betten 38812-38903 unresolved tandem in the HERV SVA exists between 184390-185163. ≩ and

FEATURES source suggests that approximately 1700 bps are missing. Location/Qualifiers /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="2" 1. .206854

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                                   BG470047 (NID:g13402322)*
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Best Local Similarity 91.: Matches 84; Conservative
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Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC Box 597, Uppsala 751 24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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                                                                                                  /translation="MSFLEQGESRSWPSRAVTTSSERSHGDQGNKASRWTRQEDVEEG
GPPGFPREGPGSRPVAESTGQEATFPKAFPLAQAAPLAFVDNPPFREDILPSDCAASAS
DSNTDHLDJGIEFSA5AASGDELGIVEEKPAFCPSFPVLLPRLGWDDELQAFGAQYI
HFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVCHLTI
TDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISPNDSLFEAVYALI
                      ALVLSPAGIDALGA"
                                      AVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
                                                                                                                                                                                                             /product="AMPK gamma subunit"
/protein_id="AAF73989.1"
/db_xref="GI:821586"
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/codon_start=1
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5471 ACATTCCGAGATTTGGCTG 5453
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                    acattccgagacttggctg 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus l (bases 1 to 227724) Rump,A., Hayes,C., Brown,S.D.M. and Rosenthal,A. Mouse chromosome 1 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227724 bp DNA linear HTG 02-APR-2001 Mus musculus chromosome 1 clone PAC510; PAC457, *** SEQUENCING IN AF336381
                                                                                                                                       h 70.3%; Score 71; DB 2; Length 227724; Similarity 93.7%; Pred. No. 1.7e-11; 74; Conservative 0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rump, A.
Direct Submission
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AF336381.1 GI:13507298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                         57663 a
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17970
32747
32847
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/organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                 /chromosome="1"
/clone="PAC510; PAC457"
55423 c 56238 g 58199 t
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         17869: contig of 17869 bp in length 17969: gap of unknown length 32746: contig of 14777 bp in length 32846: gap of unknown length 227724: contig of 194878 bp in length.
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Search completed: October 3, 2002, 14:50:23 Job time: 12143 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score di Pred. No. score distribution chance to being printed,

Disease associated	AAX06882	20	1435	30.5	30.8	9
PRKAG3 intron 4 -	AAH43683	22	1722	78.4	79.2	60
Sus scrofa PRKAG3	AAD03321	22	2022	92.7	93.6	7
Pig AMPK gamma sub	AAD03319	22	1873	92.7	93.6	6
Pig AMPK gamma sub	AAD03295	22	1867	92.7	93.6	· G
Human AMPK gamma s	AAD03320	22	2115	100.0	101	4
Human AMPK gamma s	AAD03296	22	2109	100.0	101	· tui
PRKAG3 CDNA. Homo	AAH43685	22	1647	100.0	101	N
Human AMP-activate	ABA08485	22	547	100.0	101	
Description	ID	DB	Match Length DB	Match	Score	No.
				Query		Result

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442	2 2 4 10 10 10 10 10 10 10 10 10 10 10 10 10	330 34 31 31 31	116 117 118 119 220 221	10 11 12 13 14
222222 88888	228 22 22 22 22 22 22 22 22 22 22 22 22	• co co co co co	202222222222222222222222222222222222222	30.8 29.6 89.6
	27.9 27.9 27.9 27.9 27.9	28.7 28.7 28.5 28.5 28.5 28.5 28.5 28.5 28.5		30.5 30.5 29.3 29.3 29.3
737 3125 3156 3156 3156 3156 12043	2378 2530 2588 2857 3238 4378 4732	4413 6765 7461 398 9979 13673 13673 1682 635	200 1259 1260 1260 1260 1260 12403	1467 2223 566 1326 2289 4363
22 20 21 24	22222222	23 22 23 23 23 23 23 23 23 23 23 23 23 2	24 119 20 24 23	23 22 23 23
AAH153932 AAH15387 AAV18471 AAV27969 AAA227969 AAA55996 AAA55996	ABLC6405 AAC39424 ABL21171 AAH15945 AAS77333 ABLC6404 ABL21170 AAS58263	ABL02825 ABL02824 ABL04284 ABL04284 AAF64424 AAK75448 AAK75548 AAK781195 AAC98901 AAL02279	AAS:17161 AAQ51226 AAV19135 AAV63702 AAS:17159 ABL07647 ABL07646	AAS84265 AAH14839 AAS05559 AAC37238 ABL08199 ABL08198
Human cDNA clone (Human cDNA sequenc T-cell surface ant Human CD97 protein Human CD97 nucleot Human intercellula	Drosophila melanog Arabidopsis thalia Drosophila melanog Human cDNA sequenc DNA encoding novel Drosophila melanog Drosophila melanog CDNA #939 encoding	Drosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog Novel human polynu Human immune/haema Human immune/haema Human immune/haema Human pancreatic c Human reproductive	Mouse melanocyte h Mouse MSH-R gene. Mouse melanocyte s Mouse melanocyte h Mouse melanocyte h Drosophila melanog Drosophila melanog	DNA encoding novel Human cDNA sequenc Mammalian vestibul Arabidopsis thalia Drosophila melanog Drosophila melanog

ALIGNMENTS

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RESULT
ABA08485
Human AMP-activated protein kinase subunit homologue cDNA,
                                      11-JAN-2002
                                                                         ABA08485;
                                                                                                            ABA08485 standard; cDNA; 547
                                    (first entry)
                                                                                                            ВР
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SEQ ID NO: 261.

Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopolesis regulation; tissue growth; humunomodulator; activin; inhibin, chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; lumnune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarthritic; antiarthritic; haemostatic; antiarthritic;

Homo sapiens.

cytostatic; antifungal;

vulnerary;

osteopathic; vasotropic; cardiant; virucide; antibacterial;

WO200157188-A2

ACC SCORE REPORT OF THE STATE O 05-FEB-2001; 2001WO-US03800.

PRKAG3 cDNA 21-JAN-2002 AAH43685;

(first entry)

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                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                        Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and CC invention also relates to vectors and recombinant host cells comprising a concleotide of the invention, methods of producing the novel polypeptides, and thodies against the polypeptides, methods of identifying compounds which CC polypeptides in a sample, and methods of identifying compounds which CC polypeptides of the invention have homology to known proteins, thereby CC giving an insight into their probable biological activities, and hence CC potential therapeutic applications. The polypeptides of the invention have homology to known proteins, thereby CC giving an insight into their probable biological activities, and hence CC potential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell conditions activities; thereby conditions the polypeptides of the invention may be commondulatory activity; activing the sample and the conditions of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include concerns, haematopoletic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions include conservers, haematopoletic disorders (e.g., myeloid or lymphoid cell concerns, haematopoletides included with tissue regeneration and crepair (or nucleic acids encoding them) may be used to promote wound to bacterial and fungal infections in addition to immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders (e.g., and abnormal cell can be used to augment or replace cells damaged by illness, and and cells can be used to augment or replace cells damaged by illness, and in drug contains, and in the present sequence represents a cDNA encoding a cover human polypeptides. The present sequence represents a cDNA encoding a cover human cells of the invention.
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 429; 1963pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-2000;
27-APR-2000;
                                                                                                                          (HYSE-) HYSEQ INC
                                                                     61 tatccaagatttgggcatcggcacattccgagacttggctg 101
                                                                                                                                                                                                                                    Local
                                                                                                                                             1 getcaagtteetgeacatetttggtteectgetgeeceggeecteetteetetaeegeae 60
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                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                         547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0496914.
2000US-0560875.
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                                                                                                                                                                                                                 0,:
                                                                                                                                                                                                                             Score 101; DB 22;
Pred. No. 7.9e-23;
                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                  Length 547;
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AAH43685

AAH43685 standard;

cDNA; 1647 BP

ş

Matches

101;

Similarity

100.0%; ilarity 100.0%; Conservative 0

0

Score 101; DB 2 Pred. No. 1e-22; Mismatches

DB 22; 0;

1647; 0

Indels Length

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This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71a; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R71a of a t nucleotide 1037, resulting in the amino acid substitution R71a of these variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.
Sequence 1647 BP; 346 A; 502 C; 462 G;
                                                                                                                                                                                                                                                         New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and metabor determining a risk estimate of diseases in subject by detecting
                                                                                                                                                                                                                     Disclosure; Fig 5; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                            Andersson L, Luthman
                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-2001; 2001WO-SE00765
                                                                                                                                                                                                                                                                                                                                                                                         (AREX-) AREXIS AB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Silent variation"
1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= "C1037T"
/note= "Causes R340W"
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/label= "C230G"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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KW PRXA
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   (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, primers that can detect preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, arc
                                                                                                                                                                                                                                            Claim 12; Fig
                                                                                                                                                                                               The present sequence is a cDNA encoding human adenosine monophosphate
                                                                                                                                                                                                                                                                                     New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
                                                                                                                                                                                                                                                                               myopathy
                                                                                                                                                                                                                                                                                                                                                                                                                    Andersson L, I
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18-MAY-2000;
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Gellin
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Query Match
Best Local
                                           New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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18-MAY-2000;
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| Iannuccelli N,
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 Page 65-68;
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10-SEP-1999; 99EP-0402236
18-MAY-2000; 2000EP-0401388
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cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
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CC Mutation in Prkag3 results in an altered regulation of carbobhydrate (C metabolism, particularly in skeletal muscle. PRKAG3 is useful as the present of carbobhydrate metabolism disorders such as contained with muscle metabolism (C such as myopathy and carbobhydrate metabolism disorders such as myopathy and cardiovascular diseases, to modulate AMPK (C activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic cevaluation, genetic testing and prognosis of a metabolic disorder, C preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3 are useful for detecting a dysfunctionally altered allele of PRKAG3. C useful for detecting a dysfunctionally altered allele of PRKAG3. C the expression of a functionally altered allele of PRKAG3. C heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid c encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain c of PRKAG3 and is niseful for agene therapy.
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         PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene theranv. pm 17-5 chromosome 15; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INRG ) INRA INST N
(ANDE/) ANDERSSON L
(LOOF/) LOOFT C.
(KALM/) KALM E.
                                                                                                    Pig AMPK gamma subunit muscle-specific isoform,
                                                                                                                                        13-JUN-2001
                                                                                                                                                                      AAD03319;
                                                                                                                                                                                                    AAD03319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1867 BP; 380 A; 583 C; 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment associated with energy metabolism such as diabetes, obesit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig
                                                                                                                                                                                                                                                                                 961
                                                                                                                                                                                                                                                                                                                                              901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
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Iannuccelli N,
                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                        a sequence
PRKAG3 and
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                                                                                                                                                                                                                                                                           atccaagatttgggcatcggcacattccgagacttggccg
                                                                                                                                                                                                                                                                                           atccaagatttgggcatcggcacattccgagacttggctg
                                                                                                                                                                                                                                                                                                                                        2001-244810/25
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                    standard; cDNA; 1873 BP
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                     (first entry)
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V, Gellin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; 71pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                        92.7%;
96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
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J, Le
                                                                                                                                                                                                                                                                                                                                                                                                      Score 93.6; D
Pred. No. 2.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n E,
→ Roy
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Roy P, C
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Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 T;
                                                                                                                                                                                                                                                                                                                                                                                                                       .4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DΒ
                                                                                                                                                                                                                                                                              1000
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                                                                                                      PRKAG3
                                                                                                                                                                                                                                                                                                                                                                                                                                      1867;
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        В
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Cc activity, and for restoring a normal AMPK function. PRRAG3 sequence
Cc and its functionally altered mutants are useful for the diagnostic
Cc evaluation, genetic testing and prognosis of a metabolic disorder.
Cc preferably a carbohydrate metabolism disorder. Primers that can detect
Cc a genetic polymorphic marker linked to a sequence encoding pRRAG3, are
Cc useful for detecting a dysfunction of carbohydrate metabolism resulting
Cc from the expression of a functionally altered allele of PRRAG3.
Cc renosgenic animal and host cell transformed with PRRAG3 or a
Cc heterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for
Cc screening compounds able to modulate AMPK activity. Nucleic acid
Cc encoding PRRAG3 is useful for detecting mutations in a Prkag3 gene, or
Cc in a sequence encoding the first cystathione beta synthase (CBS) domain
Cc of PRRAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                            (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in a litered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism
                                                                                                                                                                                          Sequence 1873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment associated with energy metabolism such as diabetes, obesit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12;
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        967
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Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-2000;
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18-MAY-2000;
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                 62 atccaagatttgggcatcggcacattccgagacttggctg
                                                       atccaagatttgggcatcggcacattccgagacttggccg
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                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 62-64; 71pp; English.
                                                                                                                    Conservative
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, Gellin
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                                                                                                                                                                                        BP;
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1..1395
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                                                                                                                                                                                       382 A;
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                                                                                                                              92.7%;
96.0%;
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                                                                                                                                                                                       580 C;
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                                                                                                                    0;
                                                                                                                                 Score 93.6;
Pred. No. 2
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                                                                                                                 Mismatches
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                                                                                                                                .4e-20;
                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes, obesity,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robic A,
                                                                                                                                            22;
                               101
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                                                                                                                 Indels
                                                                                                                                          Length
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                                                                                                                                            1873;
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                                                                                                              Gaps
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AAD03321
ID AAD
                                            evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrKag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                  diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of chromosome I Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as displaced to the property of the property of the present of the pres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INRG ) INRA INST NAT RECH AGRONOMIQUE (ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-1999; 99EP-0402236
18-MAY-2000; 2000EP-0401388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorec genetic testing; carbohydrate metabolism disorder; skeletal muscle;
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DB; AAE00224.
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LOOFT C.
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, Gellin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69; 71pp;
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1..1545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
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Roy P, Chai
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Sequence 2022

BP;

412 A;

623 C;

593 G;

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                                                                                                                       /number= "Intron : 987..1041
                /number= "Intron 10"
/note= "5' row:
                                                                                                                                                                                                                     /number= "Exon 96..552
                                  1689..1722
                                         /mumber= "Exon
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/number= "Intron
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/number= "Exon
1370..1522
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783..986
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737..782
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14..95
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96.0%;
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Pred. No. 2.4e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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RESULT
AAX06882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 84
                                                             DAPK-7; disease associated protein kinase; human; diagnosis; therapy; adult respiratory distress syndrome; allergy; asthma; arteriosclerosis; bronchitis; emphysema; hypereosinophilia; myocardial inflammation; pericardial inflammation; anaemia; rheumatoid arthritis; Addison's disease; AIDS; atherosclerosis; atopic dermatitis; dermatomyositis; diabetes mellitus; glomerulonephritis; gout; Grave's disease; lupus erythematosus; multiple sclerosis; myasthenia gravis; osteoarthritis; osteoporosis; pancreatitis; polycystic kidney disease; polymyositis; scleroderma; Sjorgren's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6.
           Homo sapiens
                                                      autoimmune thyroiditis; cancer;
                                                                                                                                                                                                                                            Disease
                                                                                                                                                                                                                                                                          26-APR-1999
                                                                                                                                                                                                                                                                                                                                    AAX06882 standard; cDNA; 1435
                                                                                                                                                                                                                                                                                                                                                                                                          1570 tttgggcatcggcacattccgagacttggctg 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and metabolic diseases in subject by detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AREX-) AREXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-APR-2000; 2000US-195665P
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                                                                                                                                                                                                                                                                                                                                                                                                                           70 tttgggcatcggcacattccgagacttggctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  9
                                         proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-657170/75
                                                                                                                                                                                                                                         associated protein
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                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Luthman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.4%;
91.3%;
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                                                                                                                                                                                                                                         kinase DAPK-7 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 79.2; DB Pred. No. 9e-16;
                                                                                                                                                                                                                                                                                                                                    ВΡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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C and overlapping Incyte clones 3075712/HRARNOTD1, 84220/PROSTUTO5,
C 136747/SCORNONO2, 145972 and 145802/PENITUTO1 and 1479332/CORPNOTO2.
C DAPK-7 shows 73% homology with the human foetal liver AMPK gamma
C subunit (G1 135856), and is associated with CDNA libraries which
C are immortalised or cancerous and show inflammatory or immune
C responses. The invention provides disease associated protein kinases
C DAPK-1 to DAPK-7 (see AAM88432-38) and CDNA clones encoding them (see
CC AAX06831-36 and AAX06882), as well as expression vectors, host cells,
CC agonists, antagonists and antibodies. The invention further provides
C uses of such products in the diagnosis, prevention and treatment of
CC diseases associated with cell proliferation, especially cancer or an
CC immune response (claimed). Conditions that may be treated include
CC anteriosclerosis, bronchitis, emphysema, hypereosinophilia,
myocardial or pericardial inflammation, rheumatoid arthritis,
CC Addison's disease, AIDS, anaemia, atherosclerosis, various diseases
CC of the disease, AIDS, anaemia, atherosclerosis, various diseases
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the digestive system, atopic dermatitis, dermatomyositis, diabete mellitus, glomerulonephritis, gout, Grave's disease, lupus erythematosus, multiple sclerosis, myasthenia gravis, osteoarthritis, osteoporosis, panoreatitis, polycystic kidney disease, polymyositis, scleroderma, Sjorgren's syndrome, autoimmune thyrolditis, complications of cancer, extracorporal circulation, viral, bacterial, fungal, parasitic, protozoal and helminthic infections, and trauma (disclosed). The DAPK nucleic acids are also used in a method for detection of DAPK expression levels in a
                                                                                                                                                                                                                   617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1435 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the PENITUT01 cDNA library using a computer search for amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This cDNA sequence codes for human disease associated protein kinase DAPK-7 (see AAW88438). DAPK-7 cDNA was first identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 66-67; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New disease associated protein kinases - used to stimulate proliferation and to treat the immune response and cancer % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-080952/07
P-PSDB; AAW88438.
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677 ctggatgagcttggaataggaacgtaccacaacattgc 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-1998;
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                                                               62 atccaagatttgggcatcggcacattccgagacttggc 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                            56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0878989
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265..1503
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                                                                                                                                                                                                                                                                                                                                                                                                                                           30.5%;
57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection of DAPK expression levels in a
                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30.8;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1435;
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B Ş В õ

775 ctggatgagcttggaataggaacgtaccacaacattgc

62 atccaagatttgggcatcggcacattccgagacttggc

Query Match Best Local 9

Similarity

30.5%; 57.1%;

Score 30.8; DI Pred. No. 2.3; 0; Mismatches

<u>ښ</u> BB 23; 42;

Length Indels

1467; 0; Gaps

0

Conservative

0,

Sequence 1467 BP; 416 A; 327 C;

343 G; 381 T; 0 other;

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AAS84265
ID AAS8
XX
                       CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess blodiversity
CC and to produce other types of data and products dependent on DNA and
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at fip. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 20069; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #20069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
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2000US-0649167
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RESULT 11
AAAH14839
ID AAAH148
AX AAH148
AX Human
XX Human
XX Human
XX Human
XX PP 07-FEE
XX PP 28-JUI
PP 28-JUI
PP 29-JUI
PP 29-JUI
PP 11-AU
PP 07-AU
PP 07-AU
PP 07-AU
PP 07-AU
PP 07-AU
PP 11-AU
PP 1
                   Query Match
Best Local S
Matches 56
                                                                                                                                                                                                                               sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the the third that the primers are also useful for the the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13638 and AAH13633 represent human amino acid sequences; AAB9246 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the amount of the sequences; AAB9246 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent imman amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5' end
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02-MAY-2000;
09-JUN-2000;
                                                                                                                                                         Sequence 2223 BP; 633 A; 431 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-318749/34.
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27-AUG-1999;
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                                            Similarity
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            Conservative
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A, Nagai K,
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                                                                                                                                                           and both are subjected to conditions in which the strains exhibit different geotactic behaviour. Genes that are differentially expressed the first strain relative to the second strain are then identified. Mammalian genes having substantially the same nucleic acid sequence as these modulate the mammalian vestibular system. Compounds containing these genes are used to decrease the symptoms of graviperceptive disorders such as motion sickness, vertigo, labyrinthitis, Meniere's disease, accustic neuroma, multiple sclerosis, syphilis, trauma, infection of the middle ear, exposure to ototoxic agents and epilepsy.
                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                vestibular system modulating activity. The DNA sequences can be used in method whereby a first and second strain of an invertebrate is obtained,
                                                                                                                                                                                                                                                                                                                           The sequences shown in AAS05401-AAS05661 represent DNA with mammalian
                                                                                                                                                                                                                                                                                                                                                                Claim 59; Page 144; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid having mammalian vestibular system-modulating activity useful in the treatment of disorders such as motion sickness
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalian vestibular system; invertebrate; geotactic behaviour; vertigo; graviperceptive disorder; motion sickness; labyrinthitis; syphilis; ds; Meniere's disease; acoustic neuroma; multiple sclerosis; epilepsy; trauma; infection of the middle ear; ototoxic agent exposure.
           544
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                                                             Local Similarity 68.3 hes 41; Conservative
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GCTCATCAAAGGTGACTACCTGTTCCTGCTCTTCTTCCTCTACCTCATTATCCCTGATCT 485
                 gcacatetttggttecetgetgeeeeggeeeteetteetetaeeggaetateeaagattt 72
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PR 18-JUN-1999; 99US-0139457. PR 18-JUN-1999; 99US-0139458. PR 18-JUN-1999; 99US-0139459. PR 18-JUN-1999; 99US-0139460.	18-JUN-1999; 99US-01	18-JUN-1999; 99US-01	17-JUN-1999; 99US-01	16-JUN-1999; 99US-01	14-JUN-1999; 99US-01	10-JUN-1999; 990S-01	08-JUN-1999; 99US-01	07-JUN-1999; 99US-01	04-JUN-1999: 9905-01	01-JUN-1999; 99US-01	28-MAY-1999; 99US-01	27-MAY-1999; 99US-01	24-MAY-1999; 99US-01	21-MAY-1999; 99US-01	20-MAY-1999; 99US-01	19-MAY-1999: 990S-01	14-MAY-1999; 99US-01	14-MAY-1999; 99US-01	14-MAY-1999; 99US-01	14-MAY-1999; 9908-01	07-MAY-1999; 99US-01	06-MAY-1999; 99US-01	06-MAY-1999; 990S-01	04-MAY-1999; 99US-01	30-APR-1999; 990S-01	28-APR-1999; 99US-01	23-APR-1999; 99US-01	23-APR-1999; 99US-01	19-APR-1999; 99US-0:	16-APR-1999; 99US-0:	06-APR-1999; 99US-0:	01-APR-1999; 99US-0	25-MAR-1999; 99US-0:	23-MAR-1999; 99US-0	09-MAR-1999; 99US-0	25-FEB-1999; 99US-0	XX 25-FEB-2000; 2000EP-0301439.		PD 06-SEP-2000,	PN EP1033405-A2.	XX STANTACKS CHAILAND.	Arabidoscia the Lee	metabolic pathway; promoter; to	Hybridisation assay; genetic mapping	managed cue	Arabidopsis thaliana DNA fragment con in No. 1666	DT 17-OCT-2000 (first entry)	XX XXX AVACATES	
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RESULT 14
ABL08199/c
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     ABL08199;
                    ABL08199 standard; cDNA; 2289
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990S-0151030
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990S-0154039
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99US-0150566.
99US-0150884.
99US-0151065.
                                                                                                                              29.38;
                                                                                                                    Score 29.6; DB Pred. No. 5.4; 0; Mismatches
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                   ВP
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Best Local
      WO200171042-A2
                                                                            26-MAR-2002
                                                                                           ABL08198;
                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                Claim 1;
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ABL08198/c
ID ABL08198 standard;
                                   Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGITG-ABLIGISI), expressed DNA sequences (ABLIGITG-ABLIGISI), expressed DNA sequences (ABLIGITG-ABLIGISI).
Drosophila melanogaster.
                                                                                                Drosophila melanogaster expressed polynucleotide SEQ ID NO 19076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid genes from Drosophila and interactions -
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11-JUL-2000; 2000US-0614150
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DB; ABB64096.
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llarity 68.3%;
Conservative
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                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                         Sequence 4363 BP; 1461 A; 939 C; 974 G; 989 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 19076; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000~\rm or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
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11-JUL-2000; 2000US-0614150.
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P-PSDB; ABB64095.
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B170420 BC148719 BC148719 BC148719 BC157718 BC572824 BC572824 BC572824 BC572824 BC572824 BC37282 BC37282 BC37282 BC415737 BC41573

ALIGNMENTS

REFERENCE AUTHORS SOURCE ORGANISM VERSION KEYWORDS LOCUS DEFINITION ACCESSION RESULT BI344527 FEATURES COMMENT TITLE JOURNAL source BI344527 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 572) Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid and Keele,J.W. Unpublished (2000) Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Fax: 402 762 4390 Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore and minmatch 12 options. BACKWARD: GTTTTCCCAGTCACGACG Plate: 119 row: I column: 11 Seq primer: ATTTAGGTGACACTATAG PCR PRIMERS FORWARD: AGGGAAACAGCTATGACGAT Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine EST. BI344527.1 GI:15037807 /organism="Sus scrofa" /db_xref="taxon:9823" /clone_lib="MARC 2PIG" /tissue_type="pooled" /lab_host="DH10B" /note="Vector: pCMV SPO Location/Qualifiers 572 bp mRNA linear 2PIG Sus scrofa cDNA 5', mRNA sequence pCMV SPORT6; Site_1: xbaI; Site_2: xhoI; Smith, T.P.L., Casas, E., EST 30-JUL-2001 18

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Fax: 314 286 1810
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Contact: Wilson RK
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Mammalia; Eutheria: Primates; Catarrhini; Hominidae;
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                                                                    Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

190 c 151 g 124 t 1 others
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/clone_11b-"Stratagene muscle 937209"
/tissue_type="muscle"
/dev_stage-"adult"
                                                                                                                                                                                                                  /db_xref="taxon:9606"
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/db_xref-"GDB:4643570"
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tive 0; Mismatc
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dc69g08.y1 i
5' similar i
BG037921
                                  Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; !
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
I (bases 1 to 514)
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EST.
African clawed frog.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Contact: Tadasu Shin-i
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Location/Qualifiers
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/dev_stage="stage 25"
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/clone="xL096j16"
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 Project (CGAP)
                                                                    Euteleostomi; 
; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
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                                                                                            http://image.llnl.gov
Plate: LLAM10079 row: d column:
High quality sequence stop: 691.
                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 918)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
BG027175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602295858F1 NIH_MGC_86 Homo sapiens cDNA clone
                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
                                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                              human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Xenopus laevis"
/db_xref="taxon:8355"
/clone="InMAGE:3402446"
/clone=lib="MICHD XGC Embl"
/fissue_type="embryo (stage 10)"
/lab_host="Oblide (phage resistant)"
/note="Vector: pCMV-SPORT6: Site_1: NotI; Site_2: SalI;
Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.55 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ω,
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4390238"
                                                                            Location/Qualifiers
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62.28;
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lone IMAGE:4390238
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AW147353/c
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                                                                                                                                                                                               DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clone distribution information for this library can be found through Research Genetics, visit their web page at: http://www.resgen.com/ Seq primer: -40RP from Gibco
High quality sequence stop: 409.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                WashU Xenopus EST project, 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WashU Xenopus EST project, 1999
Unpublished (1999)
Other_ESTs: daOlhll.xl
Contact: Sandy Clifton, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                     Fax:
                                                                                                                                                                                                                                                                                                                                                             Library constructed
                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; (
Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
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AW147353
AW147353.1 GI:6195249
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57; Conserv
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314 286 1810
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from 2ug of poly A+ RNA. EcoRI-XhoI cut cDNA was then ligated into Unizap-XR
                                                             /clone="XENOPUS_SOURCE_ID:xlnoc001d22"
/clone_lib="Xenopus laevis occyte"
/tissue_type="occyte (stages 5 and 6)"
/lab_host="Top-10 F'"
                                                                                                                                                             ∕organism≖"Xenopus laevis"
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/lab_host="DBH0B (phage-resistant)"
/note="Organ: bone: Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologics.
Note: this is a NH_MGC Library."
a 138 c 263 g 258 t
                                                                                                                                              /db_xref="taxon:8355"
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Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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laevis cDNA clone
to TR:070257 070257
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BASE COUNT
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Best Local :
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                                               l Similarity
52; Conserv
                                                                                                                                                                                                                                                                                                                                          Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kitayama, A., Terasaka, C., Mochii, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BJ036397
BJ036397 NIBB Mochii normalized Xenopus neurula library Xenopus laevis CDNA clone XL036d24 5', mRNA sequence.
BJ036397
BJ036397
GT07736982
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Tadasu
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed genes in X. laevis embryo
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    African clawed frog.
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                                             Conservative
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                                                                                                                                                                                                                                                                                                            tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                             /tissue_type="whole embryo"
/dev_stage="stage 15"
108 c 112 g 101 t
                                                                                                                                                                                                          library"
                                                                                                                                                                                                               /clone_lib="NIBB Mochii normalized Xenopus neurula
                                                                                                                                                                                                                                          /clone-"XL036d24"
                                                                                                                                                                                                                                                         /organism="Xenopus laevis"
/db_xref="taxon:8355"
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                                                          31.98;
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Pred. No. 47;
                                           Mismatches
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BG101440.1
                                      house mouse.
Mus musculus
                                                                                                                                  BG101440 684 bp mRNA linear EST 29-JAN-2001 uy72c12.yl McCarrey Eddy round spermatid Mus musculus cDNA clone IMAGE:3664919 5' similar to TR:09ULX8 Q9ULX8 H91620P. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                         l Similarity 61.2
52; Conservative
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                           EST
                                                                                                                         sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV914030 K. Sato unpublished cDNA library, cv. Haruna Nijo germination shoots Hordeum vulgare subsp. vulgare cDNA clone bags4d24 5', mRNA sequence.
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
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AV914030.1 GI:18209807
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Location/Qualifiers
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/clone_lib="K. Sato unpublished
Nijo germination shoots"
/tissue_type="shoots"
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137 c 141 g 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hordeum vulgare subsp. vulgare"
/cultivar="Haruna Nijo"
/db_xref="taxon:112509"
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                                                                                         GI:12596757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM488662 536 bp mRNA linear EST 07-FE. pgm2n.pk008.g21 Normalized Chicken Breast Muscle, Leg Muscle, Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus colone pgm2n.pk008.g21 5' similar to gblAACS2580.1 (U42413) 5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norv.
                          BM488662.1
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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                                                                            mRNA sequence.
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314 286 1810
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//lab_host="Diliob (phage-resist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics); excision done by E.M. Eddy, Ph.D. (National Institutes of Health, National Institute of Environmental Health Sciences). Original lambda-based library is available through ATCC, catalog #63423."

a 163 c 134 g 177 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="CD-1"
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/dev_stage="60 day"
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/clone_lib="McCarrey Eddy round
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                          GI:18609593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 CTCAAGTTCCTCAAACTCTTTATTGCAGAGGTCCCAAAGCCTGAGTTTATGGCCCGGACT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 atccaagatttgggcatcggcacattccgagacttggctg 101
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     Cogburn, L.A. and
                                                                                                                                          Gallus gallus
                                                                                                                                                                                                                                                                                                   BM487789 S95 bp mRNA linear EST 07-FEB-: pgm2n.pk005.j24 Normalized Chicken Breast Muscle, Leg Muscle, at Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk005.j24 5' similar to gb[AAC55580.1 (U42413) 5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegi
                                                       Archosauria; Aves; Neognathae; Phasianinae; Gallus.
                                                                                                               Eukaryota;
                                                                                                                                                                          chicken.
                                                                                                                                                                                                                               BM487789.1
                                                                                                                                                                                                                                                                                                                                                                                                                         BM487789
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Cogburn,L.A. and Monsonego-Ornan,E.
ESTs from Normalized Chicken Breast Muscle, Leg Muscle,
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal
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Contact: Larry A.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                (bases 1 to 595)
                                                                                                                                                                                                                                                                                 mRNA sequence.
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Location/Qualifiers
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171 c 132 g 116 t
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/strain="Commercial broiler
Strains 90 & 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Epiphyseal Growth Plate /sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Breast,leg:Embryo(d19);post-hatch(1d,1,3,5,7,9
,11 weeks):growth plate(1d,7d,14d post-hatch)"
/lab_host="E. coli EMDH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="pgm2n.pk008.g21"
/clone_lib="Normalized Chicken Breast Muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9031"
                                                                               Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
a; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                            GI:18608720
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Monsonego-Ornan, E
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Pred. No. 92;
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Length 536;

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Gaps

9

Ottawa

(pgm2n)

Leg Muscle,

subunit (Rattus norvegicus

EST 07-FEB-2002

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JOURNAL
COMMENT
                                                                                                                                            REFERENCE
AUTHORS
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Cogburn, i.A. and Nys, Y.
EST's from Normalized Chicken Reproductive Tract cDNA library-
University of Delaware and INRA, Tours-Poultry Unit Project
Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
                                                                                                                                                               chicken.
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallis.
                                                                                                                                                                                                                                                                                                                             BM440762

Byrln, pk002.19 Normalized Chicken Reproductive Tract CNA Library (pgrln, pk002.19 sqllus gallus clone pgrln., pk002.19 5' similar to gil4506061 ref | NP 002724.1| protein kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1; Protein kinase, AMP-activated, noncatalytic, gemma-1 [Homo sapiens] gi|12737489 ref|XP_006778.2| protein kinase, AMP-activated, gamma 1, mRNA sequence.
                                                                                                                                                                                                                                                                                   BM440762.1 GI:18471537 EST.
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Tel: 302-831-1335
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Location/Qualifiers
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                                                                                                                                                             1 to 647)
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/db_xref="taxon:9031"
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.11 weeks);growth plate(ld,7d,14d post-hatch)"
/lab_host="E. coli EMDH10B"
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Pred. No. 95;
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                                                                                                                                                                                   Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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AJ395115 dkf
AJ395115
AJ395115.1
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A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                        Contact: Buerstedde JM
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57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cogburn@udel.edu, www.chickest.udel.edu
Location/Qualifiers
                                                             /tissue_type="Bursa of Fabricius"
227 c 155 g 137 t
                                                                                                                /organism="Gallus gallus"
/strain="CB"
/db_xref="taxon:9031"
/clone="21c2r1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dkfz426 Gallus
                                                                                                  /clone_lib="dkfz426"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCMVSPORT6; Library made from three RNA pools from each tissue (testis 25%, ovary 25%, oviduct 50% of final RNA pool); Single pass sequence from 5'-end"

222 c 160 g 128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Testis, ovary and oviduc
/dev_stage="Various stages;embryonic,
and sexually-mature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Strain="Commercial broiler and layer"
/db_xref="taxon:9031"
/clone="pgrin.pk002.19"
/clone_lip="Normalized Chicken Reproductive Tract cDNA
Library (pgrin)"
/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. coli EMDH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Gallus gallus"
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57.08;
 30.98;
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|allus cDNA clone 21c2r1,
 31.2;
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Length 649;
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                            Local Similarity hes 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 TTGGAGGAGCTGCAGATCGGTACCTACAGCAACATCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 CTCAAGTTCCTCAAACTCTTTATTGCAGAGGTCCCCAAAGCCTGAGTTTATGGCCCGGACT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 alccaagatttgggcatcggcacattccgagacttggctg 101
                                                                                                                                                                                                                                                                                                     TTGGAGGAGCTGCAGATCGGTACCTACAGCAACATCGCCG 487
                                                                                                       H64260 413 bp
yr70cl2.rl Soares fetal liver sp
IMAGE:210646 5', mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                   Homo sapiens
                                                                                 H64260.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abdrakhmanov,I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., P., J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 758)

Abdrakhmanov *
                                                   human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heinrich-Pette-Institute
MartInistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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AJ396118 dkfz426 Gallus
AJ396118
AJ396118.1 GI:7127728
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Cellular Immunology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Gallus gallus"
/strain-"CB"
/db_xref-"taxon:9031"
                                                                                 GI:1023000
                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Bursa of Fabricius"
238 c 186 g 166 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="dkfz426"
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0; Mismatches
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                                                                                                                      spleen lNFLS Homo sapiens cDNA clone
                                                                                                                                         mRNA
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                                                                                                                                                                                                                                       Local Similarity
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                                                                                CTGGATGAGCTTGGAATAGGAACGTACCACAACATTGC
                                                                                                                                                                                                                          56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 933
High quality sequence stops:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 413)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, M., Hawkins M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 933 Std Error: 0.00
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                 132
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Location/Qualifiers
                                                                                                                                                                                                                        Conservative
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/clone_lib="Soares fetal liver spleen lNFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:3783487"
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1.1e+02;
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-395-115-1
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US-09-395-15-109-9
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IOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: PENITUT01	SSE	LENGTH: 1435	z	TELEX:	E: 415-855-0555	CATION INFORMATION:	REFERENCE/DOCKET NUMBER: DF-0321 Hg	ngs, Lucy	۲	••	ICATION NUME	PRIOR APPLICATION DATA.	70	CATION DATA:	FastSEQ	OPERATING SYSTEM: DOS	COMPUTER: TRM Compatible	READABL	ZIP: 94304	?	CA (Palo Alto	STREET: 3174 Porter Drive	TEGITO Phonoconting	ENCES:	OF INVENTION: KINASES	Ž	APPLICANT: Shah Duryi	Call Preeti	Guegler, Karl	Corley, Neil C.	Hillman,	()	AL IN	sequence 14, Application US/088/8989 Patent No. 5885803	989-14	ULT 1

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US-09-272-796-14
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US-08-878-989-14
 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14,
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                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       SOFTMARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                   TELEPHONE: 415-855-0555
                                                             LIBRARY: PENITU
CLONE: 1452972
                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                   STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                      LENGTH:
                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
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CITY: Palo Alto
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                                                                                                                                    1435 base pairs
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                                                                          PENITUT01
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Score 30.8; DB 4; Pred. No. 0.11;
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       Length 1435;
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                                                                           Best Local Similarity 58.6 Matches 51; Conservative
                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/866,97
FILING DATE: 19920410
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532347nan, Kevin E
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                       FEATURE
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: LUCITY: Chicago
CITY: Illinois
                     363 CTCATTGACGTGCTCATCTGTGGCTCCATGGTGTCCAGTCTCTGCTTCCTGGGCATCATT 422
                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cone, Roger D
APPLICANT: Mountjoy, Kathleen G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
62 atccaagatttgggcatcggcacattc 88
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                                    NAME/KEY:
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                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                 NAME/KEY:
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                                                                         Score 29.4; DB Pred. No. 0.33; 0; Mismatches
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RESULT 5
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Best Local Similarity
                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/466,906B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 30
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5849871nan, Kevin E
RECISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,154-H
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cone, Koger U
APPLICANT: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
TITLE OF INVENTION: and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                          423 GCTATAGACCGCTACATCTCCATCTTC 449
                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA to mRNA
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                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                    Score 29.4; DB 2;
Pred. No. 0.33;
                                                                                                                                                                                        Mismatches
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RESULT 6
US-09-201-746-3
; Sequence 3, Application US/09201746
; Patent No. 6268221
; GENERAL INFORMATION:
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US-08-706-281A-3
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Best Local Similarity
Matches 51; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,281A
FILING DATE: 04-SEP-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6100048nan, Kevin E
REGISTRATION NUMBER: 35,303
DEPERDENCE FOR FORMARE: 46,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6100048 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
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TITLE OF INVENTION:
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                                                                                                          423 GCTATAGACCGCTACATCTCCATCTTC 449
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                                                                                                                         62 atccaagatttgggcatcggcacattc 88
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CITY: Chicago
STATE: IL
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TELEFAX: 312-913-0002
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Chen, Wenbiao
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Using Mammalian Melanocortin Receptor Age
To Modulate Feeding Behavior in Animals
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Pred. No. 0.33;
0; Mismatches 36;
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RESULT 7
US-09-097-231-3
Sequence 3, Application US/09097231
Sentent No. 6278038
Patent No. 6278038
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
Maicolm J
                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY:
; LOCATION:
US-09-201-746-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/201, FILING DATE: 01-DEC-1998 CLASSIFICATION: 435 CLASSIFICATION: 1NFORMATION: NAME: NO. 6268221nan, Kevin E REGISTRATION NUMBER: 35,303 REPERENCE/DOCKET NUMBER: 92,11 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
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APPLICANT: Mountjoy, Kathledr
TITLE OF INVENTION: Melanocy1
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 8
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           423 GCTATAGACCGCTACATCTCCATCTTC 449
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TYPE: nucleic acid
STRANDEDNESS: single
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                                    Low, Malcolm J
TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
NUMBER OF SEQUENCES: 22
                        CORRESPONDENCE ADDRESS:
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    ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
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Pred. No. 0.33;
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LOCATION: 960..1260
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-097-231-3
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Best Local
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                      CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Wallen III
STREET: 126 E. Lincoln Avenue
                                                                              TITLE OF INVENTION: BRADYKININ B2 RECITITLE OF INVENTION: NON-HUMAN ANIMALS NUMBER OF SEQUENCES: 12
                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: <Unknown> 1: INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                     APPLICANT:
                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                 423 GCTATAGACCGCTACATCTCCATCTTC 449
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NAME: NO. 6278038nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886-C
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 1260 base pairs
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                Rahway
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STRANDEDNESS: single
New Jersey
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                                                                                                                                 Hess, John W.
Chen, Howard Y.
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Strader, Catherine D.
                                                                                                                                                                   Strader,
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58.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application GENERAL INFORMATION:
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Best Local Similarity
Matches 41; Conserv
                                                                        ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release ""
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1378 base pairs
TYPE: nucleic acid
STRANDEDNESS: 616716
                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         TITLE OF INVENTION: BRADYKININ B2 RECEPTOR MODIFIED TITLE OF INVENTION: NON-HUMAN ANIMALS NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                           APPLICANT: Hess, John W.
APPLICANT: Chen, Howard Y.
APPLICANT: Trumbauer, Myrna E.
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 0)
FILING DATE: 27-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wallen III, John W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEINIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       876 GCA 878
                                                                                                                                                                                                CITY:
STATE:
                 CLASSIFICATION:
                                    FILING DATE:
                                                                                                                                                                                                                               STREET:
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                                              APPLICATION NUMBER:
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: New Jersey
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126 E. Lincoln Avenue
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65.1%;
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                                              PCT/US95/09383
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 10
US-08-938-291A-3/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) PCT-US95-09383-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08938291A Patent No. 6117673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                             APPLICATION NUMBER: US/08/938
FILING DATE: September 26, 19:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027, 33:
FILING DATE: October 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 228/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
Communication
                                                                                                                                                                                                                                              SOFTWARE: FastSeq
CURRENT APPLICATION DATA:
                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lev, Sima
APPLICANT: Plowman, Gregory D.
APPLICANT: Schlessinger, Josep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: RDGB PROTEINS AND RETHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              876 GCA 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        816 CATGCTCCTGAATGTCGTGGGCTTCCTGCTGCCCCTGAGTGTCATCACCTTCTGCACGAT 875
                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 90071-2066
                             TELEPHONE: (213) 489-16
                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 cca 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 caagitcotgoacatotttggitcootgotgococggcootcottcotcotcocgcactat 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
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                   67-3510
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                                                                                                                                                                                                                                                                                                 IBM Compatible
                                                                                                                                                 UMBER: 60/027,337
October 11, 1996
                                                                                                                                                                                                               IUMBER: US/08/938,291A
September 26, 1997
                                                  489-1600
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65.1%;
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                                                                                228/172
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Pred. No. 1.2;
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COCATION: 79...5700

COTHER INFORMATION: \product=

OTHER INFORMATION: \channel*

US-08-336-257A-3
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US-08-336-257A-3
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Query Match
Best Local Similarity
Matches 51; Conserv
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Patent No. 5726035
GENERAL INFORMATION:
APPLICANT: Jay, Scott D
APPLICANT: Ellis, Steven B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 5489
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                TELEPHONE: (619) 238-0999
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: not 1
TOPOLOGY: not relev
MOLECULE TYPE: Genomi
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 5975 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Harpold, Michael M.
APPLICANT: Campbell, Kevin P.
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Con
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
21P: 92101-2926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0
FILING DATE: 07-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 ccaagatttgggcatcggcacattccgagacttggctg 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 5020 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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        Conservative
                                                                                                                                                                                   not relevant
E: Genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
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                                                                                                                                                                                                                 not relevant
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55.18;
                    26.18;
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   Score 26.4; D
Pred. No. 6.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  54898
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                                                                                                               "Alpha-1 subunit of animal calcium
                                 DB 1;
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   41;
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                                 Length 5975;
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   Indels
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   0
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   Gaps
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                                                                                                             Matches
                                                                                                                                       Query Match
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Patent No. 5993813
                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MAPPLICANT: GAPPLICANT: RAPPLICANT: RAPPLICANT: A
                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1734
                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: DUANE C ULMER
  837
                                                 897 CTGAGATCCCTAGACAGATTTATTTCCCAACTTCTCTCAGCCGGCTCCCTCAGGGCAAAT 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1794 CTTCGCCCTGCTGGGCATCCAGCTCTTCGGGG 1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: MIDLAND
STATE: MICHIGAN
COUNTRY: USA
ZIP: 48641-1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
              62 atccaagatttg 73
                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
STREET: P.
                                                                                                                                                                                                           STRANDEDNESS:
                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                      ENGTH:
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                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                     1984 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08822028
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                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GOURLIE, BRIAN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAPLAN, DONALD A SCHOLOM, JEFFREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANDERSON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEZES, PETER S
                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                               (517)
                                                                                                                                                                                                            double
                                                                                                                                                                                                                                                                 636-8104
ID NO: 16:
                                                                                                                       25.3%;
59.7%;
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                                                                                                                                                                                                                                                                                                                    34,941
                                                                                                       Score 25.6; DB Pred. No. 7.9; 0; Mismatches
                                                                                                          0;
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                                                                                                                                   DB 2;
                                                                                                          29;
                                                                                                                                   Length 1984;
                                                                                                          Indels
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US-08-479-285-16/c

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                                                                                                                                                                                                                                     RESULT 14
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                                                                                                                                                        Sequence 1, Application US/08481337A Patent No. 5863738 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040687
FILING DATE: 31 MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DOANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (517) 636-8104 INFORMATION FOR SEQ ID NO: 16
                                         APPLICANT: TEN DIJKE, Peter
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: MIYAZONO, Kohei
APPLICANT: SAMPATH, Kuber T.
TITLE OF INVENTION: Morphogenic Protein-Specific Cell
TITLE OF INVENTION: Surface Receptors and Uses Therefor
                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SCHOLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: DUANE C ULMER
                                                                                                                                                                                                                                                                                      837 ATCCAAGATTAG 826
                                                                                                                                                                                                                                                                                                                                                      897 CTGAGATCCCTAGACAGATTTATTTCCCCAACTTCTCTCAGCCGGCTCCCTCAGGGCAAAT 838
                                                                                                                                                                                                                                                                                                         62 atccaagatttg 73
   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1984 base pairs TYPE: nucleic acid STRANDEDNESS: double
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6207815
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                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Testa, Hurwitz & Thibeault
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Pred. No. 7.9;
0; Mismatches
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US-08-696-268B-1/c
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Best Local Similarity
              COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, vc
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,268B
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1509 base pairs
                                                                                                                                                                                                                                                                                                           APPLICANT: ICHIJO, HIDENORI
APPLICANT: NISHITOH, HIDEKI
APPLICANT: SAMPATH, KUBER T.
APPLICANT: SAMPATH, KUBER T.
TTTIE OF INVENTION: NOVEL SIGNALLING RECEPTOR FOR
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hu
STREET: 125 High St.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, Thomas C.
REGISTRATION NUMBER: 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: cDNA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CITY: Boston
STATE: MA
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ZIP: 02110
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CITY: B
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LOCATION: 1..1509
OTHER INFORMATION:
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STRANDEDNESS: single
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                                                 US/08/696,268B
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                                                                                 Version #1.30
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